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Listing first 45 summaries
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

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19: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-978-360A-407
US-10-315-664-75
US-09-895-298-66
US-09-895-298-120
US-10-262-511-184
US-10-262-511-184
US-10-844-874-20
US-09-833-245-1914
US-09-833-245-1914
US-09-833-245-1915
US-10-188-186-22
US-10-188-186-24
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Sequence 407, App
Sequence 75, Appl
Sequence 66, Appl
Sequence 120, App
Sequence 184, Appl
Sequence 20, Appl
Sequence 1914, Ap
Sequence 2115, Ap
Sequence 22, Appl
Sequence 2350, Ap
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 21, Appl
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71.8 44.7 44.1 43.9 43.9

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Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 810

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; NAME/KEY: SIGNAL ; LOCATION: -18..-1 US-10-315-664-75
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SEQ ID NO 75
LENGTH: 302
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US-09-978-360A-407
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Publication No. US20030203377A1
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Best Local Similarity 100.
Matches 302; Conservative
  Best Local Similarity
                      Query Match
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PRIOR APPLICATION NUMBER: US/09/599,360
PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: 60/113,686
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/141,032
PRIOR APPLICATION NUMBER: 60/141,032
PRIOR FILING DATE: 1999-06-25
                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: GENSET. 050CP3
CURRENT APPLICATION NUMBER: US
CURRENT FITTIN
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PRIOR FILING DATE: 1999-12-21
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EQ ID NO 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal TITLE OF INVENTION: Peptides
                                                                                                                   ORGANISM: Homo Sapiens FEATURE:
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ORGANISM: Homo Sapiens
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Score 1626; DB 14;
Pred. No. 2.4e-160;
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2.4e-160;
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; NAME/KEY: SITE
; LOCATION: (237)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-895-298-66
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Matches
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SEQ ID NO 66
LENGTH: 302
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                                                                                                                                                                                                                                        Query Match
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PRIOR FILING DATE: 2000-06-09
PRIOR ADDITORNEL DATE: 2000-06-09
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PRIOR FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PCT/US99/29950
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: 60/113,006
PRIOR FILING DATE: 1998-12-18
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CURRENT FILING DATE: 2001-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al.
TITLE OF INVENTION: 47 Human Secreted Proteins
FILE REFERENCE: PZ035P1
                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Homo sapiens
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301; Conserv
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                LRVVSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQ 180
                                                                  SVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRST
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LRVVSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQ
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                                                                                                                                                                                                      Conservative
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Pred. No. 6.2e-160;
0; Mismatches 1;
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; NAME/KEY: SITE
; LOCATION: (280)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino
US-09-895-298-120
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CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: 09/591,16
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: PCT/US99/29950
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: 60/113,006
PRIOR APPLICATION NUMBER: 60/113,006
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 60/112,809
PRIOR APPLICATION NUMBER: 60/112,809
PRIOR APPLICATION NUMBER: 60/112,809
PRIOR FILING DATE: 1998-12-17
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Best Local Similarity 99.7
Matches 301; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 231
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TYPE: PRT
ORGANISM: Homo sapiens
344
                                   301
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                                                                                                                                                                         181 VYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEBIVVYGMVSDSYCR
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                                                                                                                                                                                                                                                                                                         104 SVPDGKPLVREPCRSCAVVSSSGQMLGSGLGABIDSAECVFRMNQAPTVGFEADVGQRST
                                                                                                                                                                                                                                                                                                                            61 SVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRST
                                                                                                                                                                                                                                                                                                                                                                                  44 MKAPGRLVLIILCSVVFSAVYILLCCWAGLPLCLATCLDHHFPTGSRPTVPGPLHFSGYS
                                                                                                                                                                                                                                                                                                                                                                                                      1 MKAPGRLVLIILCSVVFSAVYILLCCWAGLPLCLATCLDHHFPTGSRPTVPGPLHFSGYS
                           TE 302
                                                                         EKSHPSVPYHYFEKGRLDECOMYLAHEQAPRSAHRFITEKAVFSRWAKKRPIVFAHPSWR
                                                                                                             EKSHPSVPYHYFEKGRLDECQMYLAHEQAPRSAHRFITEKAVFSRWAKKRPIVFAHPSWR 300
                                                                                                                                                   VYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCESIVVYGMVSDXYCR
                                                                                                                                                                                                                             LRVVSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQ
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Pred. No. 7.5e
0; Mismatches
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7.5e-160;
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APPLICANT: Stone, David J.

APPLICANT: Stone, Carol E. A.

APPLICANT: Shenoy, Suresh G.

APPLICANT: Shinkets, Richard A.

APPLICANT: Shinkets, Richard A.

APPLICANT: Rothenberg, Mark E.

APPLICANT: Leach, Martin D.

APPLICANT: Leach, Martin D.

APPLICANT: Leach, Martin D.

APPLICANT: Leach, Martin D.

APPLICANT: Berghs, Constance

FILL REFERENCE: 21402-462C

CURRENT FILING DATE: 2003-05-28

PRIOR APPLICATION NUMBER: US/10/262,511

CURRENT FILING DATE: 2001-10-02

PRIOR APPLICATION NUMBER: 60/326,483

PRIOR APPLICATION NUMBER: 60/327,917

PRIOR FILLING DATE: 2001-10-09

PRIOR APPLICATION NUMBER: 60/327,917

PRIOR APPLICATION NUMBER: 60/327,917

PRIOR APPLICATION NUMBER: 60/327,917

PRIOR APPLICATION NUMBER: 60/328,029

PRIOR APPLICATION NUMBER: 60/328,026

PRIOR APPLICATION NUMBER: 60/328,026

PRIOR APPLICATION NUMBER: 60/328,056

PRIOR APPLICATION NUMBER: 60/328,056

PRIOR APPLICATION NUMBER: 60/373,260

PRIOR FILING DATE: 2002-04-19

PRIOR APPLICATION NUMBER: 60/373,826

PRIOR APPLICATION NUMBER: 60/373,826

PRIOR APPLICATION NUMBER: 60/373,826

PRIOR APPLICATION NUMBER: 60/373,826

PRIOR APPLICATION NUMBER: 60/373,826
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                                                                                                                                                                                                                             Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 184
LENGTH: 218
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                                                                                     Query Match
Best Local S
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                                                                                                                                                                         LENGTH: 218
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                  Local Similarity
nes 218; Conserv
MLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRSTLRVVSHTSVPLLLRNYSHYFQKAR
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Peyman, John A.
Kekuda, Ramesh
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Spytek, Kimberly A.
Edinger, Shlomit R.
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Rastelli, Luca
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Anderson, David
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Malyankar, Uriel M.
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                                                             71.8%; Score 1167; DB 15; llarity 100.0%; Pred. No. 9.2e-113; Conservative 0; Mismatches 0;
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Gaps

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Sequence 1914, Application US/09833245

Publication No. US20040010134A1

GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
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APPLICANT: Yamamoto, Hirotaka
TITLE OF INVENTION: Detection and Treatment of
FILE REFERENCE: 97-186-E
CURRENT APPLICATION NUMBER: US/10/844,874
CURRENT FILING DATE: 2004-05-13
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
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US-10-844-874-20
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Best Local Similarity
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Publication No. US20040204381A1
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TYPE: PRT
ORGANISM: Rat
                                                                                                                                                                                                                                                                                                                                                                                                 180 QVYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMVSDSYC
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48.7%; Pred. No. 1.10
tive 46; Mismatches
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; ELENGTH: 305
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PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1915, Application US/09833245 Publication No. US20040010134A1 GENERAL INFORMATION:
                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 129; Conserv
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Best Local Similarity
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FILE REFERENCE: PF546FCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/256, 931
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                                                                                                                                                                                                                                                                                                           TYPE: PRT
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                                           115 VGQRSTLRVVSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTR 174
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                                                                                                                             55 HFSGYSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMVQAPTVGFEAD 114
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                           VGRMTMIRVVSHTSVPLLLKNPDYFFKEANTTIYVIWGPFRNMRKDGNGIVYNMLKKTVG
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52.7%;
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52.7%; Pred. No. 1.2e-65;
tive 48; Mismatches 65
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Pred. No. 1.2e-65;
8; Mismatches 65
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RESULT 9
US-10-188-186-22
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-186-22
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PRIOR APPLICATION NUMBER: 60/360814
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: 60/303828
PRIOR APPLICATION NUMBER: 60/323380
PRIOR FILING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-19
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SOFTWARE: Custom
SEQ ID NO 22
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Publication No. US20040029789A1
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Best Local Similarity 52.2%; Pred. No. 1.9e-65;
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CURRENT FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: 60/303046
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PRIOR APPLICATION NUMBER: 60/305673
PRIOR FILING DATE: 2001-07-16
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OR APPLICATION NUMBER: 60/361133
OR FILING DATE: 2002-03-01
OR APPLICATION NUMBER: 60/304016
OR FILING DATE: 2001-07-09
OR APPLICATION NUMBER: 60/304502
OR FILING DATE: 2001-07-11
OR APPLICATION NUMBER: 60/305262
OR FILING DATE: 2001-07-13
OR APPLICATION NUMBER: 60/373881
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                                         NDTYCKTEGYRKVPYHYYEQGR-DECDEYFLHEHAPYGGHRFITEKKVFAKWAKKHRIIF
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AHPSW 299
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                                                                     SDSYCREKSHPSVPYHYFEKGRLDECQMYLAHEQAPRSAHRFITEKAVFSRWAKKRPIVF 294
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2350
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US-10-104-047-2350
CURRENT APPLICATION NUMBER: US/10/188,186
CURRENT FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: 60/303046
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/360814
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: 60/303828
PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 60/323380
PRIOR FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/323380
PRIOR FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/361133
PRIOR FILING DATE: 2001-07-01
PRIOR APPLICATION NUMBER: 60/304016
PRIOR APPLICATION NUMBER: 60/304502
PRIOR APPLICATION NUMBER: 60/304502
PRIOR APPLICATION NUMBER: 60/304502
PRIOR PILING DATE: 2001-07-01
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US-10-188-186-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24, Application US/10188186 Publication No. US20040029789A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN VEX. 2.1
SEQ ID NO 2350
LENGTH: 305
                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local 9
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CURRENT FILING DATE: 2002-03-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: No. US20030236392A1el full length cDNA FILE REFERENCE: H1-A0105
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Anderson et al.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING
FILE REFERENCE: 21402-397C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HELIX RESEARCH INSTITUTE
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nes 128; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HY-GYINVKTQEPLQLD-CDLCAIVSNSGQMVGQKVGNEIDRSSCIWRMNNAPTKGYEED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.9%; Score 713.5; DB 1
52.2%; Pred. No. 2.4e-65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 14;
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Publication No. US20040029789A1
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Matches
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PRIOR FILING DATE: 2001-07-05
PRIOR FILING DATE: 2002-03-01
PRIOR FILING DATE: 2002-03-01
PRIOR FILING DATE: 300/303828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 21402-397C
CURRENT APPLICATION NUMBER: US/10/188,186
CURRENT FILING DATE: 2002-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Anderson et al.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Remaining Prior Application data removed - See File Wrapper or NUMBER OF SEQ ID NOS: 368
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PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 60/373881
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/305673
PRIOR FILING DATE: 2001-07-16
Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 368
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                DR APPLICATION NUMBER: 60/303828
DR FILING DATE: 2001-09-07
DR APPLICATION NUMBER: 60/32380
DR FILING DATE: 2001-09-19
DR APPLICATION NUMBER: 60/361133
DR FILING DATE: 2002-03-01
DR FILING DATE: 2002-03-01
DR FILING DATE: 2001-07-09
DR APPLICATION NUMBER: 60/304502
DR FILING DATE: 2001-07-11
DR FILING DATE: 2001-07-11
                                          OR APPLICATION NUMBER: 60/305262

IN FILING DATE: 2001-07-13

IN APPLICATION NUMBER: 60/373881

IN FILING DATE: 2002-04-19

OR APPLICATION NUMBER: 60/305673

IN FILING DATE: 2001-07-16
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nes 128; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.7%; Score 694; DB 15; llarity 49.6%; Pred. No. 2.7e-63; Conservative 48; Mismatches 66
                   See File Wrapper or PALM
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RESULT 13
US-10-097-340-189
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                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/097,34
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-26
PRIOR PRIOR PRIOR ON UMBER: 60/3276,026
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR APPLICATION NUMBER: 60/324,967
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                                                      PRIOR APPLICATION NUMBER: 60/311,732
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR APPLICATION NUMBER: 60/323,580
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For TITLE OF INVENTION: Assessment, Prevention, and Therapy of FILE REFERENCE: MRI-030
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                                       PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                  FILING DATE: 2001/09/26
APPLICATION NUMBER: 60/311,732
FILING DATE: 2001-08-10
                  OF SEQ ID NOS:
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Karen GLATT
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Robert C. BAST, Jr.
Karen LU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosemarie SCHMANDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peter VEIBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ami SEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Steve G.
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Shubhangi KAMATKAR
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for Windows
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-340-189
                                                                        ; ORGANISM: Homo sapiens
US-10-094-749-2441
                                                                                                                                                                        APPLICANT: NAGAHARI, KENUI
APPLICANT: NAGHARI, KENUI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 189
LENGTH: 336
Query Match 39.3%; Score 639.5; DB 14; Length 336; Best Local Similarity 47.9%; Pred. No. 1.4e-57; Matches 125; Conservative 44; Mismatches 89; Indels 3;
                                                                                                                                          SOFTWARE: PatentIn
SEQ ID NO 2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2441, Application US/10094749 Publication No. US20030219741A1
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Best Local Similarity 47.9%;
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                                                                                                           TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 GRTYRTLLQLTRMYPGLQVYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 MYDAPTRGYGRDVGNRTSLRVIAHSSIQRILRNRHDLLNVSQGTVFIFWGPSSYMRRDGK 182
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OTSUKI, 12...
WAKAMATSU, AI
SATO, HIROYUKI
SATO, SHIZUKO
TOWN-I
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TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
NAGAHARI, KENJI
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SUGIYAMA, 10...
TETSUJI
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YAMAMOTO, JUN-ICHI
TSONO, YUUKO
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; TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
FEATURE:
OTHER INFORMATION: Incyte ID
US-10-288-252-11
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US-10-288-252-11
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                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/288,252
CURRENT FILING DATE: 2002-11-04
PRIOR APPLICATION NUMBER: PCT US01/30424
PRIOR FILING DATE: 2000-10-9-28
PRIOR PILING DATE: 2000-11-21
PRIOR PILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: US 60/249,639
PRIOR FILING DATE: 2000-11-16
PRIOR PILING DATE: 2000-11-16
PRIOR PILING DATE: 2000-11-09
                                                                                                                SOFTWARE: PERL
SEQ ID NO 11
LENGTH: 336
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Publication No. US20030143686A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
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                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/238,481 FILING DATE: 2000-10-06
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HAFALIA, April J.A.
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LEE, Ernestine
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                                                                                                                                                         Program
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                    No.
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Database :
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                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
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DB seq length: 2000000000
A_Geneseq_23Sep04:*
1: geneseqp1990s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
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1626
1 MKAPGRLVLIILCS
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| 25                 | 24       | 23                 | 22       | 21       | 20                 | 19       | 18       | 17                 | 16       | 15       | 14                 | 13       | 12                 | 11                 | 10                 | 9        | 8        | 7                  | 6        | 5                  | 4        | w        | 2                  | 7                  | No.          | Result |
|--------------------|----------|--------------------|----------|----------|--------------------|----------|----------|--------------------|----------|----------|--------------------|----------|--------------------|--------------------|--------------------|----------|----------|--------------------|----------|--------------------|----------|----------|--------------------|--------------------|--------------|--------|
| 639.5              | 639.5    | 639.5              | 677.5    | 694      | 713.5              | 714.5    | 716.5    | 716.5              | 716.5    | 716.5    | 716.5              | 716.5    | 716.5              | 726.5              | 1159               | 1167     | 1622     | 1622               | 1626     | 1626               | 1626     | 1626     | 1626               | 1626               | Score        |        |
| 39.3               | 39.3     | 39.3               | 41.7     |          | 43.9               | 43.9     | 44.1     | 44.1               | 44.1     | 44.1     | 44.1               | 44.1     | 44.1               | 44.7               | 71.3               | 71.8     | 99.8     | 99.8               | 100.0    | 100.0              | 100.0    | 100.0    | 100.0              | 100.0              | Match        | Query  |
| 336                | 336      | 336                | 305      | 318      | 305                | 305      | 363      | 305                | 305      | 305      | 305                | 305      | 305                | 305                | 218                | 218      | 345      | 303                | 302      | 302                | 302      | 302      | 302                | 302                | Match Length |        |
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| ADA54873           | ABG96367 | AAE10705           | ADC26195 | ADC26199 | ADB64196           | ADC26197 | AAE21617 | ADL78433           | ADL78432 | ABG65166 | ABG65165           | AAE21595 | AAE21578           | ADD47791           | ADN62987           | ADA05824 | AAB24495 | AAB24441           | ADP19151 | ADD47793           | AAB75350 | AAB61614 | AAB28674           | AAB25764           | B            |        |
|                    |          |                    |          |          |                    |          |          |                    |          |          |                    |          |                    |                    |                    |          |          |                    |          |                    |          |          |                    | į                  |              |        |
| Ada54873 Human pro | Human    | Aae10705 Human sia | Human    | Human    | Adb64196 Human pro |          | Human    | Adl78433 Albumin f | Album:   | Human    | Abg65165 Human alb | Human    | Aae21578 Human gen | Add47791 Rat Prote | Adn62987 Human NOV | Human    | Human    | Aab24441 Human sec |          | Add47793 Human Pro | Human    | Human    | Aab28674 Human car | Aab25764 Human sec |              |        |

This sequence represents a human secreted protein amino acid sequence. The invention relates to sequences AAA87725-A87774 which encode human secreted proteins AAB25763-B2512. The proteins include signal peptides. Included in the invention are a host cell containing one of the cDNA sequences, and a purified antibody capable of binding to one of the secreted proteins. Also contained in the invention are methods for

Claim 9; Fig 12; 306pp; English.

procedures.

Polynucleotides and polypeptides encoding proteins with signal peptides, useful in diagnostic, forensic, gene therapy and chromosome mapping

WPI; 2000-442637/38. N-PSDB; AAA87726.

Bougueleret L,

Dumas J,

Duclert A;

| 45       | 44       | 43       | 42       | 41       | 40       | 39       | 38       | 37       | 36       | 35       | 34        | 33       | 32       | 31        | 30       | 29       | 28       | 27       | 6                                       |
|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|-----------|----------|----------|-----------|----------|----------|----------|----------|---|
| 537      | 537      | 537      | 537      | 537      | 537      | 537      | 537      | 537      | 537      | 537      | 537       | 537      | 537      | 537       | 537      | 548.5    | 595.5    | 633.5    | 000.0                                   |
| 33.0     | 33.0     | 33.0     | 33.0     | 33.0     | 33.0     | 33.0     | 33.0     | 33.0     | 33.0     | 33.0     | 33.0      | 33.0     | 33.0     | 33.0      | 33.0     | 33.7     | 36.6     | 39.0     |   |
| 299      | 299      | 299      | 299      | 299      | 299      | 299      | 299      | 299      | 299      | 299      | 299       | 299      | 299      | 299       | 299      | 256      | 246      | 275      |   |
| თ        | σ        | σ        | σ        | σ        | σ        | σ        | თ        | Q        | ტ        | 0        | σ         | თ        | 4        | 4         | w        | 4.       | 4        | 4        | ţ                                       |
| ABO02791 | ABO08739 | ABU92662 | ABU96231 | ABR68178 | ABU89929 | ABU82808 | ABU99569 | ABR65629 | ABR66239 | ABU84365 | ABU88050  | ABU58502 | AAU29126 | AAB66105  | AAY99356 | AAM41144 | AAM40096 | AAM41882 | 12400000                                |
| Abo02791 | Abo08739 | Abu92662 | Abu96231 | Abr68178 | Abu89929 | Abu82808 | Abu99569 | Abr65629 | Abr66239 | Abu84365 | Abu88050  | Abu58502 | Aau29126 | Aab66105  | Aay99356 | Aam41144 | Aam40096 | Aam41882 |   |
| Human    | Human    | Human    | Novel    | Human    | Novel    | Human    | Human    | Human    | Human    | Human    |           | Human    | Human    | Protein c | Human    | Human    | Human    | Human    | , ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,, |
| 860      | 860      | sec      | hun      | sec      | hun      | PRC      | sec      | sec      | 8ec      | sec      | ELIA<br>T | PRC      | PRC      | E .       | PRC      | g        | gg       | ğ        |   |

## ALIGNMENTS

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RESULT 1
AAB25764
                                                                                                                                                                                                                                                                                                         Human; secreted protein; forensic procedure; gene therapy; chromosome mapping; cancer; autoimmune disease; cardiovascular disorder; cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis; brain disorder; skeletal muscle disorder; eye disorder; obesity; mitochondriocytopathy; diabetes; atherosclerosis; Alzheimer's disease; neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia; septic shock; impotence.
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB25764;
                                                                                                                                                                                                                                             29-JUN-2000.
                                                                                                                                                                                                                                                                       WO200037491-A2.
                                                                                                                                                                                                                               20-DEC-1999;
                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein SEQ ID #76.
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25-JUN-1999;
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RESULT 2
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Matches 302;
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                                                                                                                                                                                                                                                                                                                     Human; carbohydrate-modifying enzyme; CME; antidiabetic; immunosuppressive; anti-HIV; antiinflammatory; antianaemic; antiasthmatic; antiarteriosclerotic; antithyroid; hepatotropic; nephrotropic; antigout; thyromimetic; neuroprotective; osteopatiantiarthritic; antipsoriatic; uropathic; ophthalmological; dermatological; antiulcer; cytostatic; virucide; antibacterial; fungicide; protozoacide; tranquiliser; vulnerary; diabetes; autoimmune disorder; inflammatory disorder; infection.
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                                                                     20-APR-2000; 2000WO-US010882
                                                                                                                                                                                                    WO200063351-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human carbohydrate-modifying enzyme Incyte ID
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Pred. No. 1.2e-160;
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05-APR-2001

(first

entry)

AAB61614

standard;

protein; 302

Human protein HP03380.

Human; hydrophobic domain; immune deficiency; autoimmune disorder; allergy; tissue growth; regeneration; wound healing; burn; tumour;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a human carbohydrate-modifying enzyme (CME). CME CC polynucleotides and polypeptides are useful for treating and diagnosing CC diseases associated with CME such as diabetes, autoimmune/inflammatory CC disorders such as AIDS, Addison's disease, adult respiratory distress syndrome, allergies, anaemia, asthma, atherosclerosis, autoimmune CC thyroiditis, bronchitis, cholocystitis, contact dermatitis, Crohn's CC disease, emphysema, erythroblastosis fetalls, glomerulonephritis, Good CC pasture's syndrome, gout, Grave's disease, Hashimoto's thyroiditis, CC multiple sclerosis, myasthenia gravis, osteoarthritis, osteoporosis, CC gancreatitis, polymyositis, psoriasis, Reiter's syndrome, arthritis, collis, uveitis, werner syndrome, systemic lupus erythematosus, ulcerative CC colitis, uveitis, and extracorporeal circulation, viral, bacterial, fungal CC parasitic, protozoal, and helminthic infections, trauma, or cancer. CME, or its catalytic or immunogenic fragment, is useful for drug screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel carbohydrate modifying enzyme polypeptides and polynucleotides for diagnosis, treatment, and prevention of carbohydrate metabolism disorders, autoimmune/inflammatory disorders, and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 302 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 67-68; 75pp; English.
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                            TE 302
                                                                                          EKSHPSVPYHYFEKGRLDECQMYLAHEQAPRSAHRFITEKAVFSRWAKKRPIVFAHPSWR
                                                                                                                                                         VYTFTERMMAYCDQIFQDETGKURRQSGSFLSTGWFTMILALELCEEIVVYGMVSDSYCR
                                                                                                                                                                                                                                                                                                     SVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRST
TE 302
                                                                    EKSHPSVPYHYFEKGRLDECOMYLAHEOAPRSAHRFITEKAVFSRWAKKRPIVFAHPSWR
                                                                                                                                       VYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMVSDSYCR
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Pred. No. 1.2e-160;
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The present invention relates to human proteins (AAB61608-AAB61617) and their coding sequences (AAF28679-AAF28698). The proteins of the present invention have hydrophobic domains and can be used for the treatment of various immune deficiencies and disorders, such as severe combined immunodeficiency (SCID), multiple sclerosis, rheumatoid arthritis, autoimmune pulmonary inflammation, graft-versus-host disease and Guillain -Barre syndrome. The proteins may also be useful in the treatment of allergic reactions and conditions, such as asthma and in regulation of haematopoiesis or lymphoid cell deficiencies. The proteins may also have utility in compositions used for bone, cartilage, tendon and/or nerve tissue growth or regeneration as well as wound healing and in the treatment of burns. The proteins may be used in the treatment of thrombolytic and haemostatic conditions, treatment of periodontal disease and in other tooth repair processes. Other uses include treatment of thrombolytic and haemostatic conditions, treatment of thrombolytic and haemostatic conditions, viruses,
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Matches 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human proteins with hydrophobic domains, useful for the treatment of immune disorders, tumors, allergic conditions, thrombosis and microbial
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infection.
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TE 302
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to 49 Secreted proteins and the clencoding them. The protein and nucleic acids may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate protein expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 302 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 Secreted proteins and the nucleic acids encoding them, useful in therapy and for detecting similar sequences in samples.
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21-DEC-1999;
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29-JAN-2004 ADD47793; ADD47793 standard; protein;

302 AA

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subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. spen the sequence presented is a human protein (shown in Table 2 of the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
 Query Match
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Matches 302
                                                                                                                                                                                                                                                                                                                                                                                                                                    kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a bit to be a comparation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic cons spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page; 1017pp;
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                                                                       Sequence 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New composition comprising two or more isolated polypeptides, useful preparing a medicament for treating pain in an animal.
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                                                                                                       ftp.wipo.int/pub/published_pct_sequences.
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The invention relates to human cDNA sequences that encode human secreted proteins. The invention also relates to an antibody that specifically binds to a polypeptide of the invention and a method of binding the polypeptide to an antibody. The polymucleotides are useful for expressing the entire secreted proteins which they encode and for distinguishing human tissues and cells from non-human tissues and cells, and for distinguishing between human tissues and cells that do or do not express the polymucleotides comprising the cDNAs. The polymucleotides and polypeptides are useful in forensic procedures or diagnostic procedures to identify individual and the polymucleotides are useful in forensic procedures or diagnostic procedures.

for expressing

or diagnostic procedures resulting from abnormal

Claim 2;

SEQ ID

NO 407; 113pp; English.

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21-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression of the genes corresponding to the cDNAs. The sequences are also useful in gene therapy to control or treat genetic diseases. This sequence represents a human secreted polypeptide of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at sequence.html.
                                                                                                                                                                                                                                                 Human; secreted protein; cytostatic; antianaemic; antidiabetic; antiinflammatory; ophthalmological; antirheumatic; antiarthritic; antipsoriatic; antiangiogenic; cardiant; anti-HIV; nootropic; neuroprotective; antimicrobial; antiparkinsonian; cancer; immune system disorder; apptiosis; hyperproliferative disorder; cardiovascular disorder; apptiosis; neurological disease; infectious disease; wound healing; chromosome 9.
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Shi Y, Lafleur DW, Olsen HS,
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Forty seven human nucleic acids encoding secreted proteins, treatment, prevention and diagnosis of cancers, disorders of system, angiogenesis disorders, neurological diseases and hyperproliferative disorders.
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Claim 11; Page 482-483; 562pp; English.

human secreted proteins given in AAB24437 to AAB24604. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities include: cytostatic; antianaemic; antidiabetic; antiinflammatory; ophthalmological; antirheumatic; antiarrhritic; antipsoriatic; antiangiogenic; cardiant; anti-HIV; nootropic; neuroprotective; antimicrobial and antiparkinsonian. Human secreted protein polymucleotides, polypeptides, antagonists and/or agonists may be useful in treating, preventing, and/or diagnosing other disorders and/or conditions such as: (a) cancers; (b) disorders of the immune system; (c) anglogenesis disorders; (d) disorders of the immune system; (e) cardiovascular disorders; (f) diseases hyperproliferative disorders; (e) cardiovascular disorders; (f) diseases appotosis; (g) neurological diseases; and (h) infectious diseases. They are also used to promote wound healing.

AAA78372 to AAA78380 and AAB24436 represent sequences used in the exemplification of the present invention The polynucleotide sequence given in AAA78381 to AAA78432 encode the

Sequence 303 AA;

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AAB24495 standard; protein; 345

Human secreted protein sequence encoded by gene σı SEQ ID NO:120

neuroprotective; antimicrobial; antiparkinsonian; cancer; immune system disorder; angiogenesis; hyperproliferative disorder; Human; secreted protein; cytostatic; antianaemic; antidiabetic; antiinflammatory; ophthalmological; antirheumatic; antiarthriti antipsoriatic; antiangiogenic; cardiant; anti-HIV; nootropic; cardiovascular disorder; apoptosis; antiarthritic;

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Matches 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infectious diseases. They are also used to promote wound AAA78372 to AAA78380 and AAB24436 represent sequences use exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Forty seven human nucleic acids encoding secreted proteins, useful in the treatment, prevention and diagnosis of cancers, disorders of the immune system, angiogenesis disorders, neurological diseases and hyperproliferative disorders.
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18-DEC-1998;
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H.
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                                                                               EKSHPSVPYHYFEKGRLDECQMYLAHEQAPRSAHRFITEKAVFSRWAKKRPIVFAHPSWR
                                                                                                                           VYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMVSDXYCR
                                                                                                                                            VYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMVSDSYCR
                                                                                                                                                                                          LRVVSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQ
                                                                                                                                                                                                            LRVVSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQ
                                                                                                                                                                                                                                                        SVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRST
                                                                                                                                                                                                                                                                                   SVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRST
                                                            EKSHPSVPYHYFEKGRLDECQMYLAHEQAPRSAHRFITEKAVFSRWAKKRPIVFAHPSWR
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                              302
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98US-0113006P.
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                                                                                                                                                                                                                                                                                                                                                                                                      99.8%;
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Shi Y,
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, Lafleur DW, Olsen
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Pred. No. 3.9e-160;
                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   promote wound healing. sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soppet DR, Ni J;
sen HS, Florence
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Ort T, G Ji W, Mi Shimkets

2003-381626/36. DB; ADA05823.

יות, Gangolli

thson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, turajan M, Spytek KA, Edinger SR, Ellerman K, Malyanka T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catt W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy mkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, en AJ, Gangolli EA, Rieger DK, Spaderna SK;

Malyankar UM; M, Catterton SG

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Dipippo

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Guo

Patturajan Smithson G,

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, cancer or dyslipidemia, and in chromosome mapping, tissue typing

obesity,

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RESULT 9
ADA05824
ID ADA05824
ID ADA05824
AC ADA058
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AC Human
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24-OCT-2001;
29-OCT-2001;
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16-MAY-2002;
16-MAY-2002;
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17-MAY-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiparkinsonian; antilipaemic;
metabolic disorder; diabetes; o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-NOV-2003
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2002US-0373815P
2002US-0373815P
2002US-0373826P
2002US-0373884P
2002US-0373884P
2002US-038103PP
2002US-038103PP
2002US-0381042P
2002US-0381042P
2002US-0381642P
2002US-0381642P
2002US-0383636P
2002US-0383635P
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2001US-0327917P.
2001US-0328029P.
2001US-0328044P.
2001US-0328849P.
2001US-0328444P.
2001US-0330142P.
2001US-0330142P.
2001US-0341058P.
2001US-0341058P.
2001US-034525P.
2001US-034525P.
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disorder;

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RESULT 10
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AC ADN62
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DT 01-JT
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DT Human
XX
KW human
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human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
                                  Human NOV44a
                                                                    01-JUL-2004
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                                                                                                      ADN62987
                                                                                                                                         ADN62987 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                     13
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22-APR-2002;
16-MAY-2002;
16-MAY-2002;
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19-APR-2002;
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19-APR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anorexia; cancer; cancer-associated cachexia; neurodegenerative Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X; wasting disorder.
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17-MAY-2002;
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) MALYANKAR U M.
) ORT T.
                                    MILLER C E.
RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHENOY S G.
                                                                                                                                                                                                      SMITHSON G
MILLET I.
PEYMAN J A
KEKUDA R.
AGEE M L.
BERGHS C.
DIPIPPO V A.
                                                                                                        GORMAN L.
ZERHUSEN B 1
ANDERSON D 1
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                               ROTHENBERG
                                                                                           CATTERTON E.
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                      LEACH M D.
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2001US-0330142p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activity of NOVX polypeptides. For example, NOVX polypeptides and polynucleotides may be used to treat disorders associated with decreased expression or activity of NOVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polynucleotides and complementary sequences may also be used as NNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of NOVX. The continuous continuous polypeptides and antagonists may also be used to modulate NOVX polypeptide expression and activity of NOVX polypeptides. The anti-NOVX polypeptide antibodies agonists and antagonists may also be used as onlypeptides and polynucleotide expression and activity of NOVX polypeptides and polynucleotides may be used in this way to prevent, disease anoversia. Center as accertance of NOVX in samples. NOVX polypeptides and treat: metabolic disorders, diabetes, obesity, infectious and security of nove of sease anoversia. Center as the carbavia center is the disorders, diabetes, obesity, infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, haematopoietic disorders, and the various dyplipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated NOVX polypeptides and polynucleotides. NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patturajan
                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo turajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UI T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Cattert W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; mkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dijen A, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2004-213931/20.
181
                                                                                                                                                                                                                                              145
                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                al Similarity
217; Conserv
                                                                                                                                                                                                                                                                                                                                               85 MLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRSTLRVVSHTSVPLLLRNYSHYFQKAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GANGOLLI E A.
RIEGER D K.
SPADERNA S K.
  AHEQAPRSAHRFITEKAVFSRWAKKRPIVFAHPSWRTE
                              AHEQAPRSAHRFITEKAVFSRWAKKRPIVFAHPSWRTE
                                                                                                                                RQSGSFLSTGWFTMILALELCEEIVVYGMVSDSYCREKSHPSVPYHYFEKGRLDECQMYL
                                                                                                                                                                                                DTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQVYTFTERMMAYCDQIFQDETGKNR
                                                                                                                                                                                                                              DTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQVYTFTERMAYCDQIFQDETGKNR
                                                                                                                                                                                                                                                                                              MLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRSTLRVVSHTSVPLLLRNYSHYFQKAR
                                                                                                 RQSGSFLSTGWFTMILALELCEEIVVYGMVSDSYCREKSEPSVPYHYFEKGRLDECQMYL
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
                                                                                                                                                                                                                                                                                                                                                                                                                  71.3%;
99.5%;
                                                                                                                                                                                                                                                                                                                                                                                          Score 1159; DB 0,
Pred. No. 4.2e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
  218
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 218;
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Malyankar UM;
M, Catterton E;
                                                                                                                                                                                                                                                                                                                                                                                                0,
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RESULT 11

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14 SVVFSAVYILLCCWAGLFLCLATCLDHHFFT-----GSRFTVPGFLHFS------GY

Matches

Local 146;

Similarity

44.7%; Score 726.5; DB 48.7%; Pred. No. 9e-67;

46; Mismatches

85; 7;

Gaps

59

Length Indels 23;

Conservative

Sequence 305

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JADD47791

ADD47791

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AC

ADDX

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Ratt

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RATT

                                                                                                       CC kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal CC subjected to pain, a method for identifying a compound which regulates CC the expressed in an animal subjected to pain, a method for identifying a compound which regulates CC compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a CC compound that regulates the activity of one or more of the specification, a method for identifying a compound useful in treating CC pain and a pharmaceutical composition comprising the one or more CC modulates or their antibodies. The polynucleotide or the compound that composition comprising the one or more CC injury (CCI) and spared nerve injury (chung), chronic constriction conjury (CCI) and spared nerve injury (chung), chronic constriction conjury (CCI) and spared nerve injury (chung) an animal (e.g. gene CC the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed conspecification, but was obtained, in electronic form directly from WIPO at francisc intinging a constriction at the constriction of the printed appecification, but was obtained, in electronic form directly from WIPO at francisc constriction at the constriction of the printed appecification, but was obtained, in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention discloses a composition comprising two or more isolated is or human polynucleotides or a polynucleotide which represents a fragmen derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a polynucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New composition comprising two or more isolated polypeptides, useful preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENBANK; NP_061996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-NOV-2001; 2001US-0333347P
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01-NOV-2001; 2001US-0346382P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003016475-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat Protein NP_061996, SEQ ID NO 13487.
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                                                                              ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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RESULT 12
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ID AAB21
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XX Human
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AAD34106-AAD34144 represent cDNAs corresponding to 17 human secreted protein genes, and AAE21578-AAE21616 represent the proteins they encode AAE21617-AAE21627 represent human secreted protein fragments. The genes
                                                                                                                                                                                      Seventeen nucleic acid molecules encoding human secreted proteins, useful for treating and preventing cancer, immune disorders (e.g. Addison's disease, and allergies), and cardiovascular disorders (e.g. myocardial
                                                                                                                                                                                                                                                                                                                                                                                                           Rosen
Olsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; proliferative disorder; cancer; tumour; AIDS; foetal abnormality; developmental; haematopoietic disorder; kidney; skin; immune system; cardiovascular; angiogenic; gastrointestinal; endocrine; pregnancy-related disorder; cognitive; neurological; autoimmune disease; inflammation; allergy; rheumatoid arthritis; Alzheimer's disease; asthma; Parkinson's disease; schizophrenia; psoriasis; sepsis; atherosclerosis; Parkinson's disease; schizophrenia; psoriasis; sepsis; atherosclerosis; diabetes; infection; wound healing; vulnerary; chemotaxis; food additive;
                                                                                                                                                                                                                                                                                                   WPI; 2002-315684/35.
N-PSDB; AAD34106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
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                                                                                                          Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                  Fiscella M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME
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                                                                                                          Page 437-438; 483pp; English.
                                                                                                                                                                                                                                                                                                                                                                                  Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                       Komatsoulis
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p, Ebner R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC and their corresponding secreted proteins are useful for preventing, cc treating or ameliorating medical conditions, e.g., by protein or gene cc therapy. Pathological conditions can be diagnosed by determining the camount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the clique developing products for the diagnosts or treatment of cancer, cc proliferative disorders, tumours, foetal and developmental abnormalities, diseases (rheumatoid arthritis) inflammation, allergies, neurological cdisorders (Alzheimer's diseases of the immune system, ALDS, autoimmune cdisorders (Alzheimer's disease, Parkinson's disease), cognitive disorder, cc schizophrenia, asthma, skin disorders (psoriasis), sepsis, diabetes, catherosclerosis, cardiovascular disorders, angiogenic disorders, disorders, gastrointestinal disorders, pregnancy-related disorders, cendocrine disorders, and infections. The proteins can also be used to aid comburn, to maintain organs before transplantation, for supporting cc cognate ligands or binding partners, and in chemotaxis, and can be used can a food additive or preservative to modify storage properties. The present sequence represents a human secreted protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 129
                                                                                                                                                   Human; secreted protein; proliferative disorder; cancer; tumour; AIDS; foetal abnormality; developmental; haematopoletic disorder; kidney; skin, immune system; cardiovascular; angiogenic; gastrointestinal; endocrine; pregnancy-related disorder; cognitive; neurological; autoimmune disease; inflammation; allergy; rheumatoid arthritis; Alzheimer's disease; asthma
                                                                                                                                                                                                                                                                                                16-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                 AAE21595 standard; protein; 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 305
                                                                                                                       diabetes; infection; wound
                                                                                                                                                                                                                                                              Human
                                                                                                                                       Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295
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                                                                                                                                                                                                                                                            gene 1
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129; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HY-ĠYINVKTQEPLQLD-ĊDLĊAIVŚNŚĠQMVĠQKVĠNĖIDRSSĊIWRMNAPTKĠYEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AHPSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VGQRSTLRVVSHTSVPLLLKNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HFSGYSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                        THPNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NDTYCKTEGYRKVPYHYYEQGR-DECDEYFLHEHAPYGGHRFITEKKVFAKWAKKHRIIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDSYCREKSHPSVPYHYFEKGRLDECQMYLAHEQAPRSAHRFITEKAVFSRWAKKRPIVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IYPNAQIYVTTEKRMSYCDGVFKKETGKDRVQSGSYLSTGWFTFILAMDACYGIHVYGMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGRMTMIRVVSHTSVPLLLKNPDYFFKEANTTIYVIWGPFRNMRKDGNGIVYNMLKKTVG
                                                                                                                                         disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
A
                                                                                                                                                                                                                                                              encoded secreted protein HE9PR39,
                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.18; 52.78;
                                                                                                                       schizophrenia; psoriasis;
wound healing; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     core 716.5; DB red. No. 1e-65; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                        sepsis; atherosclerosis;
chemotaxis; food additiv
                                                                                                                                                                                                                                                              SEQ ID NO:67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305;
                                                                                                                                                           disease; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         u
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                                                                                                                                                                                                             skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             294
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Peptide

Location/Qualifiers
1. .30
/label= Signal\_peptide

Homo sapiens

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AAD34106-AAD34144 represent cDNAs corresponding to 17 human secreted protein genes, and AAE21578-AAE21616 represent the proteins they encode. AAE21617-AAE21627 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing. The therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the candidate the sample of the candidate they are most highly expressed, and include developing products for the diagnosis or treatment of cancer, proliferative disorders, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune disorders (Alzhelmer's diseases, Parkinson's disease), cognitive disorder, schizophrenia, asthma, skin disorders (psoriasis), sepsis, diabetes, kidney altergase cartification, astronarisation, and control of the cartification disorders, anglogenic disorders, kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. The present sequence represents a human secreted protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seventeen nucleic acid molecules encoding human secreted proteins, useful for treating and preventing cancer, immune disorders (e.g. Addison's disease, and allergies), and cardiovascular disorders (e.g. myocardial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Olsen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 129; Conserv
                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305
                             SDSYCREKSHPSVPYHYFEKGRLDECQMYLAHEQAPRSAHRFITEKAVFSRWAKKRPIVF
                                                                                                                       IYPNAQIYVTTEKRMSYCDGVFKKETGKDRVQSGSYLSTGWFTFILAMDACYGIHVYGMI
                                                                                                                                                                  MYPGIQVYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMV
                                                                                                                                                                                                                                                      VGRMTMIRVVSHTSVPLLLKNPDYFFKEANTTIYVIWGPFRNMRKDGNGIVYNMLKKTVG
                                                                                                                                                                                                                                                                                                 VGQRSTLRVVSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTR
                                                                                                                                                                                                                                                                                                                                                                                 HY-GYINVKTQEPLQLD-CDLCAIVSNSGQMVGQKVGNEIDRSSCIWRMNAPTKGYEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                HFSGYSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEAD 114
NDTYCKTEGYRKVPYHYYEQGR-DECDEYFLHEHAPYGGHRFITEKKVFAKWAKKHRIIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 450-451; 483pp; English.
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Moore PA, Wei P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.1%;
ilarity 52.7%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48;
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, Ebner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 716.5; DB
Pred. No. 1e-65;
8; Mismatches
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Duan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 305;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                       238
                                                                                                                                                                                      234
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129;

55 HFSGYSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEAD

65;

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Gaps

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HY-GYINVKTQEPLQLD-CDLCAIVSNSGQMVGQKVGNEIDRSSCIWRMNNAPTKGYEED

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RESULT 14
ABG65165
ID ABG65
XX ABG65
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XX ABG65
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DE Human
XX Albur
KW Albur
KW Cytcos
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KW Cytcos
KW Cytcos
KW Immur
KW Osterc
XX Osterc
XX Homo
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Best Loc
Matches
                                                             Query Match
                                                                                                                                                                                 The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin fusion proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New fusion protein for treating disease e.g. albumin fused to a therapeutic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-APR-2000; 2000US-0229358P
25-APR-2000; 2000US-0199384P
21-DEC-2000; 2000US-0256931P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Albumin fusion protein; therapeutic protein X; human albumin; HA; human serum albumin; HSA; cancer; reproductive disorder; digestive disorder; immune disorder; endocrine disorder;
                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 1796-1797; 2102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-APR-2001; 2001WO-US011988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neuroprotective; osteopathic; ant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      haematopoietic disorder; neural disorder; connective disorder; cytostatic; antiinfertility; antiinflammatory; antiulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human albumin fusion protein #1840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG65165 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI
                           Local
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                                  Similarity
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44.1%;
llarity 52.7%;
Conservative 40
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Score 716.5; DB
Pred. No. 1e-65;
B; Mismatches
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therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, digstive disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Alpheimer's, Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis, schizophrenia), and comnective disorders (e.g. osteoporosis, arthritis).

ABG63326-ABG65518 represent albumin fusion proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-APR-2000; 2000US-0229358P.
25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Albumin fusion protein; therapeutic protein X; human albumin; HA; human serum albumin; HSA; cancer; reproductive disorder; human serum albumin; HSA; cancer; reproductive disorder; disorder; immune disorder; endocrine disorder; haematopoietic disorder; neural disorder; connective disorder; cytostatic; antiinfertility; antiinflammatory; antiulcer; immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic; neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
                                                                                                                                                                                                                                                                                          New fusion protein for treating disease e.g. albumin fused to a therapeutic protein.
                                                                                                                                                                                                                                                        Claim 1; Page 1797-1798; 2102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-APR-2001; 2001WO-US011988
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                                                                                                                                                                                                                  The present invention relates to albumin fusion
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                                 SDSYCREKSHPSVPYHYFEKGRLDECQMYLAHEQAPRSAHRFITEKAVFSRWAKKRPIVF
                                                                   VGQRSTLRVVSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTR 174
                                                                                                                                                        HFSGYSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEAD
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Title: Perfect score:

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Scoring table:

1825181 segs,

Gapop 10.0 , BLOSUM62

Cad45372 homo sapi Q8cam7 m mus muscu Aah55737 mus muscu Bac31331 m 7 days

Q9bvh7 homo sapien Cad45372 homo sapi

Q8ndv1 homo sapien Q9jhp2 mus musculu Q6zxy7 brachydanio

Cag26703 Q6zxy6

pan troglod pan trogl brachydan Aah59363 homo sapi Q6zyp1 pan troglod Cag25676 pan trogl

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Total number of hits satisfying chosen parameters:
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1: uniprot_sprot:*
2: uniprot_trembl:*
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RY SubMed=14702039; DOI=10.1038/ng1285;

RX DubMed=14702039; DOI=10.1038/ng1285;

RX Ota T., Suzuki Y., Nishi T., Shibahara T., Tanaka T., Ishii S.,

RX Alamantsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

RX Makamatsu A., Hayashi K., Sato H., Nahamura Y.,

RX Alamantsu A., Hayashi K., Yasuda T., Isono Y., Nakamura Y.,

RX Alamara K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,

RX Nijaratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,

RX Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,

RX Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,

RX Sugawara M., Takahashi M., Katanda K., Yokoi T., Furuya T., Kikawa E.,

RX Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,

RX Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,

RX Yamazaki K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,

RX Fujimori K., Tanai H., Kimata M., Watanabe M., Hotuta T.,

RX Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,

RX Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
                                                                                                                                                                                                                                                                            TISSUE=Lung;
Yoshida A.;
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(209H4F1; Q9NWU5; Q9UKU1; Q9ULB9; Q9Y3G3; Q9Y3G4;

28_FEB-2003 (Rel. 41, Created)

28_FEB-2003 (Rel. 44, Last sequence update)

05_JUL-2004 (Rel. 44, Last sequence update)

Alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3-N-acetyl-
galactosaminide alpha-2,6-sialyltransferase (EC 2.4.99.7) (NeuAc-
alpha-2,3-Gal-beta-1,3-GalNAC-alpha-2,6-sialyltransferase) (ST6GalNAC

IV) (Sialyltransferase 7D) (Sialyltransferase 3C).
                                                                                                                                                                                                                                     "N-acetylgalactosaminide alpha2,6-sialyltransferase.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
[4] RDJ
                                                                                                                                                                                                                                                                                                                                  TISSUB-Fetal liver;

Kim K.-W., Kim K.-S., Do S.-I., Kim C.-H., Lee Y.-C.;

Kim K.-W., Kim K.-S., Do S.-I., Kim C.-H., Lee Y.-C.;

"Molecular cloning of NeuAcalpha2, 3Galbeta1, 3GalNAc alpha2, 6-

sialyltransferase cDNA from human fetal liver.";

Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20517254; PubMed=11062056;
Harduin-Lepers A., Stokes D.C., Steelant
Krzewinski-Recchi M.A., Vallejo-Ruiz V.,
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Delannoy P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Eutheria; Primates; Catarrhini; Hominidae; Homo.
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S17E HUMAN
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W.F.A., Samyn-Petit Zanetta J.P., Auge (

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Score

Match Query

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1436 1047.5 1047.5 740 740

1597 1479 1479 1476 1476 1476 1452 1452 1452 1453 1439

Database

Post-processing: Minimum Match

Minimum DB Maximum DB

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RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Takemoto M., Kawakami B.,
RA Fujimori Y., Koniyama M., Tashiro H., Tanigami A., Pujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT Complete sequencing and characterization of 21,243 full-length human
CT. CDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan K., Farmer A.A., Rubin G.M., Hong L.,
A Hopkins S., Loquellano K., Farmer A.A., Rubin G.M., Hong L.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Tomeration and initial analysis of more than 15,000 full-length human
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Extensive gene order differences within regions of conserved synteny between the Fugu and human genomes: implications for chromosomal evolution and the cloning of disease genes.";

Hum. Mol. Genet. 8:1313-1320(1999).

"I-FUNCTION: Involved in the biosynthesis of ganglioside GDIA from GM1B. Transfers CMP-NeuAc with an alpha-2,6-linkage to GalNAc residue on NeuAc-alpha-2,3-Gall-beta-1,3-GalNAC of glycoproteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.
                                                                                                                                                                                                                           between
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                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   galactosaminyl-R.
PATHWAY: Glycosylation.
SUBCELLULAR LOCATION: T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity).
CATALYTIC ACTIVITY: CMP-N-acetylneuraminate + N-acetyl-alpha-
CATALYTIC ACTIVITY: CMP-N-acetysl-(1->3)-N-acetyl-D-
neuraminyl-(2->3)-beta-D-galactosyl-(1->3)-N-acetyl-D-
galactosaminyl-R = CMP + N-acetyl-alpha-neuraminyl-(2->6)]-N-acetyl-D-
palactosyl-(1->3)-[N-acetyl-alpha-neuraminyl-(2->6)]-N-acetyl-D-
neuraminyl-(2->6)]-N-acetyl-alpha-neuraminyl-(2->6)]-N-acetyl-D-
                                                                                                                                                                                                                                                                                                                                                                                       similarity).
TISSUE SPECIFICITY: Ubiquitous.
                                                                                                                                                                                                                                                                                                                                                            SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                       Belongs to
                                                                                                                  rmatics Institute. There are no rest institutions as long as its content
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N., Sano S., Suzuki O., Suzuki O.,
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EMBL; AF127142; AAF00102.1; -.
EMBL; AB035172; BAA87034.1; -.
EMBL; AK000600; BAA91281.1; -.
EMBL; BC036705; AAH36705.1; -.
EMBL; SC036705; AAH36705.1; -.
EMBL; Y17460; CAB44353.1; -.
EMBL; Y17461; CAB44554.1; -.
Genew; HGNC:17846; SIATTD.
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CARBOHYD
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                      Oriol
                                                                               Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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Pfam; PF00777; Glyco_transF_29; T.
Glycoprotein; Glycosyltransferase; Golgi stack; Signal-anchor;
                                                                                                                   Name=siat7D;
                                                                                                                             Alpha-2,6-sialyltransferase
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           Submitted (APR-2004) to the
                                  Harduin-Lepers A.,
                                             SEQUENCE
                                                                    NCBI_TaxID=9598;
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AJ646870; CAG26699.1;
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Lumenal, catalytic (Potential).

By similarity.

N-linked (GlCNAc. . .) (Potential).

S -> T (in Ref. 1).

ST -> QA (in Ref. 2).

F -> L (in Ref. 4).

M; 08A4CDC749A6D783 CRC64;
                                                                                                                              Last sequence update)
Last annotation update)
ST6GalNAc IV (Fragment).
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            EMBL/GenBank/DDBJ databases
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Matches 296; Conserv
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CAG26699;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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23-APR-2004 (TrEMBLrel. 27, Last sequence update)
23-APR-2004 (TrEMBLrel. 27, Last annotation update)
23-APR-2004 (TrEMBLrel. 27, Last annotation update)
Alpha-2,6-sialyltransferase ST6GalNAc IV (Fragment)
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Pred. No. 5.5e-137;
2; Mismatches 4;
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Pred. No. 5.5e-137;
2; Mismatches 4;
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Catarrhini; Hominidae;
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Best Local S
Matches 272
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GO; GO:0047290; F: (alpha.N-acetylneuraminyl-2,3-beta-galactos...
GO; GO:0016757; F.transferase activity, transferring glycosyl...
InterPro; IPR001675; Glyco_transf_29.
Pfam; PF00777; Glyco_transf_29: 1.
Glycosyltransferase.
Glycosyltransferase; Transferase.
SEQUENCE 302 AA; 34226 MW; 6C48E3977DA96733 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Beta-galactosamide alpha-2,6-sialyltransferase (EC Name-siat7b; Synonyms-ST6GALNAC-IV;
                                                                                                                                                                                                                                                                                                                                                                           Submitted (JAN-2004) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metāzoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa (Pig).
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                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                  LRVVSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQ
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                                                      EKSHPSVPYHYFEKGRLDECQMYLAHEQAPRSAHRFITEKAVFSRWAKKRPIVFAHPSWR
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Pred. No. 3.1e-
10; Mismatches
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3.1e-126;
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CAF05851
ID CAF05851;
CAF05851;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DT 0
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Best Local S
Matches 272
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Beta-galactosamide alpha-2,6-sialyltransferase (EC
Name=siat7b; Synonyms=st6GalNAc-IV;
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Q704X4;
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                                                                                                                                                 SEQUENCE FROM N.A. Harduin-Lepers A.,
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Mammalia; Eutheria;
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                                                EMBL;
                                                                          Submitted (JAN-2004) to the
                                                                                                                       Oriol R.;
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                                                                                                                                                                                                                                                                                                   Bovinae; Bos
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           GO:0047290;
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   CAF05850.1; -. F: (alpha-N-acetylneuraminyl-2,3-beta-galactos.
                                                                                                                                                     Martinez-Duncker
                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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Pred. No. 3.1e-126;
.0; Mismatches 20;
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Sus.
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Best Local Sim
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Beta-galactosamide alpha-2,6-sialyltransferase (EC
SIAT7B OR ST6GALMAC-IV.
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                                                                                                                                                                                                                                                                                                                                                               "Phylogeny of sialyltransferases.";
submitted (JAN-2004) to the EMBL/Ge
EMBL; AJ620651; CAP05850.1; -
Glycosyltransferase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                  SVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRST
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Pred. No. 6.3e-
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Q8C3J2;
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MEDLINE=20530913; PubMed=11076861;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
                                                                                                                                                                                                                                                                      Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shiba
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected
prepare full-length cDNA libraries for rapid discovery
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Mammary
The FANTOM Consortium,
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STRAIN=C57BL/6J; TISSUE=Mammary gland;
MEDLINE=21085660; PubMed=11217851;
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STRAIN=C57BL/6J; TISSUE=Mammary gland;
MEDLINE=99279253; PubMed=10349636;
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01-JUN-2003 (TEMBLrel. 24, Last annotation update)
Mus musculus 10 days lacttation, adult female mammary gl
full-length enriched library, clone:D730030H08
product:sialyltransferase 7 ((alpha-N-acetylneuraminyl
betsgalactosyl-1.3)-N-acetyl galactosaminide alpha-2,6
sialyltransferase) D, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUB=Mammary gland; MEDLINE=20499374; PubMed=11042159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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01-MAR-2003
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Submitted (Apr-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AK085730; BAC39523.1; -.

RGO; GO:0005794; C:Golgi apparatus; IEA.

GO; GO:0005794; C:Golgi apparatus; IEA.

GO; GO:0008373; F:sialyltransferase activity; IEA.

GO; GO:000873; F:sialyltransferase activity; IEA.

GO; GO:0006466; P:protein amino acid glycosylation; IEA.

DR GO:0006466; P:protein amino acid glycosylation; IEA.

GO; GO:00077; Glyco_transf_29; I.

Pfam; PP00777; Glyco_transf_29; I.
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Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
NCBI_TaxID=10090;
[1]
                                                                                                                               Q6PHP9
Q6PHP9;
05-JUL-2004 (TrE
05-JUL-2004 (TrE
05-JUL-2004 (TrE
Siat7d protein (
Name=Siat7d;
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Fukuda S., Furuno M., Hanagaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J;
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a K., Akimura T
                                                    Chordata;
Rodentia;
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Pred. No. 8
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V. Tagami P
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CSTRAIN=C57BL/6; TISSUE=Brain;

RX MEDLINE=22388257; PubMed=12477932;

RX MEDLINE=22388257; PubMed=12477932;

RX MEDLINE=22388257; PubMed=12477932;

RX MEDLINE=2388257; PubMed=12477932;

RX MILLSHOP S.F., Peingold E.A., Granner C.M., Schat N.K.,

RX Alleschul S.F., Zeeberg B., Buertow K.H., Casavant T.L., Schaetz T.E.,

RX Alleschul S.F., Joarian K., Farmer A.A., Rubin G.M., Hong L.,

RX Alleschul S.F., Loquellano N.B., Bonaldo M.F., Casavant T.L., Schaetz T.E.,

RX Aschards S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RX Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,

RX Alleschul S.F., Woerley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RX Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RX Alleschey R.W., Touchman J.W., Green E.D., Dickson M.C.,

RX Alleschey R.W., Touchman J.W., Green E.D., Dickson M.C.,

RX Alleschey R.W., Touchman J.W., Green E.D., Dickson M.C.,

RX Alleschey R.W., Touchman J.W., Green E.D., Dickson M.C.,

RX Allesche R.W., Touchman J.W., Green E.D., Dickson M.C.,

RX Allesche R.W., Touchman J.W., Green E.D., Dickson M.C.,

RX Allesche R.W., Suchmutz J., Myers R.M., Butterfield Y.S.,

RX Allesche R.W., Suchmutz J., Myers R.M., Schein J.E.,

RX Allesche R.W., Suchmutz J., Myers R.M., Schein J.E.,

RX Allesche R.W., Suchmutz J., Myers R.M., Schein J.E.,

RX Allesche R.W., Suchmutz J., Myers R.M., Schein J.E.,

RX Allesche R.W., Suchmutz J., Myers R.M., Schein J.E.,

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RX Allesche R.W., Suchmutz J., Myers R.M., Schein J.E.,
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Best Local S
Matches 269
                    AAH56451 PRELIMINARY;
AAH56451;
02-MAR-2004 (TrEMBLrel. 27, C.
02-MAR-2004 (TrEMBLrel. 27, L.
02-MAR-2004 (TrEMBLrel. 27, L.
51417d protein (Fragment).
SIAT7D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Generation and initial analysis of more than 15,000 full-length and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
    Mus musculus
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BC056451; AAH56451.1; -.
Pro; IPR001675; Glyco_trans_29.
PF00777; Glyco_transf_29; 1.
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  (Mouse)
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Last sequence update)
Last annotation updat
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Pred. No. 9.5e-124;
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RESULT 11
SI7D MOUSE
ID SI7D M
AC Q9R2E6
DT 28-FEB
DT 28-FEB
DT 05-JUL
DE Alpha-

STANDARD; PRT; 360 AA.

Q9R2B6; O88725; Q9JIE0; Q9QUP9; Q9R2B5;

Q9FEB-2003 (Rel. 41, Created)

28-FEB-2003 (Rel. 41, Last sequence update)

05-JUL-2004 (Rel. 44, Last annotation update)

Alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3-N-acetyl-

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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Wagney D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Wagney D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Butterfield Y.S.,
RA Rodriguez A.C., Grimwood J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Tones S.J., Marra M.A.;
Jones S.J., Marra M.A.;
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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STRAIN=C57BL/6; TISSUE=Brain;
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MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Mammalia; Eutheria;
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                                                                                                                            EKSPRSVPYHYFEKGRLDECOMYRLHEOAPRSAHRFITEKAVFSRWAKKRPIVFAHPSWR
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Pred. No. 9.5e-124;
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EMBL; Y15780; CAB43514.1; -.
EMBL; Y15780; CAB43515.1; -.
EMBL; Y15779; CAB43507.1; -.
EMBL; Y15779; CAB43508.1; -.
EMBL; X15779; CAB43508.1; -.
EMBL; AJ007310; CAA07446.1; -.
EMBL; AJ0057; CAB93948.1; -.
MGD; MGI:1341894; Siat7d.
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"Comparative analysis of the genomic structures and promoter activities of mouse Siaa2,3Galb1,3GalNacGalNacGa,6-sialyltransferase genes (ST6GalNAc III and IV): Characterization of their Sp1 binding.",

J. Biochem. 127:399-409(2000).

-I- FUNCTION: Involved in the biosynthesis of ganglioside GD1A from GM1B. Transfers CMP-NeuAc with an alpha-2,6-linkage to GalNac residue on NeuAc-alpha-2,3-Gal-beta-1,3-GalNAc of glycoproteins and glycolipids. Prefers glycoproteins to glycolipids.

-I- CATALYTIC ACTIVITY: CMP-N-acety1-neuraniate + N-acety1-alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lee Y.-C., Kaufman M., Kitazume-Kawaguchi S., Kono M., Takashima S., Kurosawa N., Liu H., Pircher H., Tsuji S.; "Molecular cloning and functional expression of two members of mouse NeuAc-alpha-2,3Gal-beta-1,3GalNAc GalNAc-alpha2,6-sialyltransferase family, ST6GalNAc III and IV.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ICR; TISSUE=Brain; MEDLINE=99223522; PubMed=10207017;
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alpha-2,3-Gal-beta-1,3-GalNAc-alpha-2,6-sialyltransferase) (ST6GalNAc
IV) (Sialyltransferase 7D).
InterPro; IPR001675; Glyco_trans_29.
Pfam; PF00777; Glyco_transf_29; I.
Alternative splicing; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20198252; PubMed=10731711;
Takashima S., Kurosawa N., Tachida Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neuraminyl-(2->3)-beta-D-galactosyl-(1->3)-N-acetyl-D-galactosaminyl-R = CMP + N-acetyl-alpha-neuraminyl-(2->3)-beta-D-galactosyl-(1->3)-[N-acetyl-alpha-neuraminyl-(2->6)]-N-acetyl-D-galactosyl-(1-)-N-RATHWAY: Glycosylation.

SUBCELLULAR LOCATION: Type II membrane protein. Golgi (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Sialyltransferase
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IsoId=Q9R2B6-1; Sequence=Displayed;
Name=2; Synonyms=Long 1;
IsoId=Q9R2B6-2; Sequence=VSP_001788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isoforms;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Comment=Experimental confirmation may be lacking for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chem. 274:11958-11967(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synonyms=Short;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata;
Rodentia;
           Glycoprotein; Glycosyltransferase; Golgi stack;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIFICITY,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTERNATIVE
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; Murinae; Mus
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q6ZXZO;
05-JUL-2004
05-JUL-2004
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DISULFID
CARBOHYD
                                                               NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Alpha-2,6-sialyltransferase ST6GalNAc IV (Fragmen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARSPLIC
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                                                                                                                                                    EMBL; AJ646871; CAG26700.1;
GO; GO:0016757; F:transferase activity,
InterPro; IPR001675; Glyco trans 29.
Pfam; PF00777; Glyco_trans 29; I.
                                                                                                                                                                                                                                                                                                             STRAIN-Wistar;
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q6ZXZ0
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                                                                                                                               Glycosyltransferase;
                                                                                                                                                                                                                                           Submitted (APR-2004) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                    02101
                                                                                                                                                                                                                                                                                    Harduin-Lepers A., Martinez-Duncker I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat)
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302
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134
193
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                                                                  A,
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                                                             302
; 34332 MW;
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283
193
58
                                                                                                                                                                                                                                                                                                                                                                                                 Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40773
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  88.3%;
88.1%;
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88.1%;
                                                                                                                                    Transferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytoplasmic (Potential).
Signal-anchor for type II membrane
protein (Potential).
Lumenal, catalytic (Potential).
By similarity.
N-linked (GlCNAc. . .) (Potential).
Missing (in isoform 3).
/FTIG-VSP 001787.
MEHYVTCWRLKLLSWPYFLIWICLSLAS -> MSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1439; DB 1;
Pred. No. 1.7e-122;
1; Mismatches 25;
Score 1436;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PQRTPIRSF (in isoform 2).
/FTId=VSP 001788.
7CF4101B8FDA369A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi
Sciurognathi; Muridae; Murinae; Ra
                                                                  FA3F65E9B0C25886 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   302 AA.
                                                                                                                                                                                               transferring glycosyl.
                                                                                                                                                                                                                                                                                      Mollicone R.,
  DB 2;
.6e-122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
                                                                                                                                                                                                                                             databases
                      Length 302;
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                                                                                                                                                                                                                                                                                      Delannoy
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RESULT 13
CAG26700
ID CAG26
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Best Local S
Matches 266
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23-APR-2004 (TrEMBLrel. 27, Created)
23-APR-2004 (TrEMBLrel. 27, Last sequence update)
23-APR-2004 (TrEMBLrel. 27, Last annotation update)
23-APR-2004 (TrEMBLrel. 27, Last annotation update)
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Phylogeny of sialyltransferases.";
Submitted (APR-2004) to the EMBL/GenBank/DDBJ
EMBL; AJ646871; CAG26700.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
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                                                                                                                                                               LRVVSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VYTFTERMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMVSDSYCR
                              VYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMVSDSYCS
                                                          VYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMVSDSYCR
                                                                                                                                     LRVISHTSVPLLLRNYSHYFQHARDTLYVVWGQGRHMDRMLGGRTYRTLLQLTRMYPGLQ
                                                                                                                                                                                                                                             SVPDGKPLTRELCHSCAVVSSSGQMLGSGLGAQIDGAECVLRMNQAPTVGFEEDVGQRST
                                                                                                                                                                                                                                                                                 SVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRST
                                                                                                                                                                                                                                                                                                                                                       MKARGRLLLLILCSITISALYVFLCCWACLPLCLATCLDPHLPAPPRSTVPGPLHFRGYS
                                                                                                                                                                                                                                                                                                                                                                                MKAPGRLVLIILCSVVFSAVYILLCCWAGLELCLATCLDHHFPTGSRFTVPGGLHFSGYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AK 302
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302 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34332 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.3%; Score 1436; DB 2;
88.1%; Pred. No. 2.6e-122;
tive 11; Mismatches 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FA3F65E9B0C25886
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                                                                              CAF05852;
(2-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Beta-galactosamide alpha-2,6-sialyltransferase (EC ST6GALNAC-IV OR SIAT7B.
                           Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
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Query Match
Best Local S
Matches 195
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Beta-galactosamide alpha-2,6-sialyltransferase (EC Mame=slat7b; Synonyms=STGGALNAC-IV;
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q704X2;
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EMBL; AJ620653; CAF05852.1; -.

GO; GO:0047290; F: (alpha-N-acetylneuraminyl-2,3-beta-galactos.

GO; GO:0016757; F:transferase activity, transferring glycosyl.

InterPro; IPR001675; Glyco trans

Pfam; PF00777; Glyco transferase.

Glycosyltransferase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harduin-Lepers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9031;
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les 195; Conserv
                                                                          173
 233
                                     246
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ERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMVSDSYCREKSHP
                                                                                                                                                                     HTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQVYTFT
                                                                                                                                                                                                                                               KPLVREPCRSCAVVSSSGOMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGORSTLRVVS
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                                                                                                                                                    HTSVPLLLRNQPYFFQQSRDTIYVIWGPSRKWSREKGGPTHRALLRVLEWYPRLQLYTLT
                                                                                                                                                                                                                            KPLRRAPCRRCAVVSSSGQMLGSHLGREIDGQECVLRMNHAPTAGFEEDVGTRSTVRVVS
                                                                          EEKWAYCDDVFQNETGKNRLKSGSFLSTGWFTMILAMELCEHICVFGMVSDSYCREKNHS
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66.3%; Pred. No. 6e-87;
tive 33; Mismatches
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PRELIMINARY;

PRT;

289

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Aves; Neognathae;

Chordata;

Craniata; Vert; Galliformes;

Vertebrata; Euteleostomi; mes; Phasianidae; Phasiani

Phasianinae;

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                                                                                                                                                                                                                               Query Match 64.4%; Score 1047.5; DB 2; Length 289; Best Local Similarity 66.3%; Pred. No. 6e-87; Matches 195; Conservative 33; Mismatches 55; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                        Gallus.
NCBI_TaxID=9031;
[1]
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Martinez-Duncker I., Mollicone R., Delannoy P.,
Oriol R.;
Oriol R.;
"Phylogeny of silyltransferases.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ620653; CAF05852.1; -.
Glycosyltransferase; Transferase.
Glycosyltransferase; Transferase.
Glycosyltransferase; Transferase.
246 SVPYHYFEKGRLDECQMYLAHEQAPRSAHRFITEKAVFSRWAKKRPIVFAHPSW 299
                                            6 RLVLIILCSVVFSAVYILLCCWAGLFLCLATCLDHHFFTGSRFTVFGFLHFSGYSSVFDG
                                                                                                                                                                                                                                                       DB 2; Length 289;
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Search completed: December 10, 2004, 18:25:12 Job time : 194 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No.
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR 79:*
1: pir1:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                   hypothetical prote
protein T23G18.14
N-glycan alpha 2,8
gal-beta(1-3/1-4)G
                                                                                                                                beta-galactoside a
GM3 alpha-2,8-sial
                                                                                                                                                                    beta-galactoside a
alpha-N-acetylneur
alpha-N-acetylgala
                                                                                                                                                                                                                           alpha-N-acetylgala
Gal beta 1,3(4)Glc
Gal beta 1,3(4)Glc
                                                                                                                                                                                                                                                                                 alpha-2,8-sialytra
alpha-2,8-polysial
Gal beta 1,4 GlcNA
                                                                                                              alpha-N-acetylneur
                                                                                                                                                                                                                                                                                                                                            polysialyltransfer 
Gal beta 1,3GalNAc
                                                                                                                                                                                                                                                                                                                                                                                    beta-galactoside
                                                                                                                                                                                                                                                                                                                                                                                                    CMP-NeuAc-GM3 alph
alpha-N-acetylneur
                                                                                                                                                                                                                                                                                                                                                                                                                                       beta-galactoside a
Gal-beta-1,3GalNac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             beta-galactoside
beta-galactoside
beta-galactoside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               beta-galactoside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302
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| 45  | 44                | 43                 | 42                 | 41                 | 40                 | 39                 | 38                 | 37                 | 36                 | 35                 | 34                 | 33                 | 32                 | 31                | 30                 |
|---|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|
| 84  | 84                | 85.5               | 86                 | 86.5               | 88                 | 88.5               | 89                 | 93.5               | 97                 | 126                | 127.5              | 134                | 137.5              | 139.5             | 140.5              |
| 5.2   | 5.2               | 5.3                | 5.3                | 5.3                | 5.4                | 5.4                | 5.5                | 5.8                | 6.0                | 7.7                | 7.8                | 8.2                | 8.5                | 8.6               | 8.6                |
| 642   | 322               | 461                | 618                | 517                | 480                | 883                | 431                | 990                | 255                | 470                | 222                | 387                | 404                | 375               | 376                |
| <u>, , , , , , , , , , , , , , , , , , , </u> | N                 | N                  | N                  | N                  | N                  | N                  | N                  | N                  | N                  | N                  | N                  | N                  | N                  | N                 | N                  |
| S52111  | S66766            | B41313             | 148914             | S32169             | S14394             | A96662             | B37802             | D83706             | T52352             | T49278             | B54898             | JE0364             | A54871             | I39169            | JC5600             |
| uromodulin precurs                            | probable membrane | probable transposa | protein-tyrosine k | hypothetical prote | bindin precursor - | hypothetical prote | crtX protein - Erw | lantibiotic mersac | hypothetical prote | hypothetical prote | STX protein - huma | lactosylceramide a | Gal beta-1, 3GalNA | sialyltransferase | alpha-N-acetylneur |

## ALIGNMENTS

C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jul-1995 #sequence\_revision 07-Jul-1995 #text\_change 09-Jul-2004
C;Accession: B54420
R;Lee, Y.C.; Kojima, N.; Wada, E.; Kurosawa, N.; Nakaoka, T.; Hamamoto, T.; Tsuji, S.
J. Biol. Chem. 269, 10028-10033, 1994
A;Title: Cloning and expression of cDNA for a new type of Galbetal,eGalNAc alpha2,3-sial; A;Reference number: A54420; MUID:94193584; PMID:8144500
A;Accession: B54420

beta-galactoside alpha-2,3-sialyltransferase (EC 2.4.99.4) ST3GalA.2 - rat C;Species: Rattus norvegious (Norway raf)

RESULT B54420

| · .   |  |  |                  |  |   |
|---|--|--|------------------|--|---|
| RESULT 2  JC5251  beta-galactoside alpha-2,3-sialyltransferase (EC 2.4.99.4) - human  C;Species: Homo sapiens (man)  C;Date: 19-Mar-1997 #sequence revision 25-Apr-1997 #text_change 09-Jul-2004  C;Accession: JC5251; G01021  R;Kim, Y.J; Kim, K.S; Kim, S.H; Kim, C.H; Ko, J.H.; Choe, I.S.; Tsuji, S.; Lee, Y.C.  Biochem. Biophys. Res. Commun. 228, 324-327, 1996  A;Title: Molecular cloning and expression of human Gal beta 1,3GalNAc alpha 2,3-sialytrar  A;Reference number: JC5251; MUID:97079181; PMID:8920913  A;Status: nuclecic acid sequence not shown  A;Molecule type: mRNA | QY 230 VYGMVSDSYCREKSHPSVPYHYFEKGR 256 | Db 192 GSRTTHHFMYDESAKNLPANVSFVLVPFKALDLMWIASALSTGQIRFTYAPV 243  Qy 170 LQLTRMYPGLQVYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEBIV 229 | 59<br>132<br>116 | Query Match 14.7%; Score 239; DB 2; Length 350;<br>Best Local Similarity 34.3%; Pred. No. 2.2e-13;<br>Matches 71; Conservative 24; Mismatches 80; Indels 32; Gaps 8; | A;ACCEBBION: B54470 A;Status: preliminary A;Molecule type: mRNA A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-350 <lee> A;Cross-references: UNIPROT:Q11205; GB:X76988; NID:g475225; PIDN:CAA54293.1; PID:g475226 C;Superfamily: beta-galactoside alpha-2,3-sialyltransferase C;Keywords: glycosyltransferase; transmembrane protein</lee> |

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C;Species: Mus musculus (house mouse)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A54420
R;Lee, Y.C.; Kojima, N.; Wada, E.; Kurosawa, N.; Nakaoka, T.; Hamamoto, T.; Tsuji, S.
J. Biol. Chem. 269, 10028-10033, 1994
A;Title: Cloning and expression of cDNA for a new type of Galbetal,eGalNAc alpha2,3-sial
A;Reference number: A54420; MUID:94193584; PMID:8144500
A;Accession: A54420
A;Ctession: A54420
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-350 <LEE>
A;Cross-references: UNITROT:Q11204; GB:X76989; NID:g475203; PIDN:CAA54294.1; PID:g475204
C;Superfamily: beta-galactoside alpha-2,3-sialyltransferase
C;Keywords: glycosyltransferase; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: ST3(0)-II
C;Superfamily: beta-galactoside
C;Keywords: glycosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X96667; NID:g1235530
C;Comment: This enzyme catalyzes the transfer of sialic acid from CMP-NeuAc to the term
substrate preference for glycolipid than for O-linked oligosaccharides of glycoproteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-350 <KIM>
A;Cross-references: UNIPROT:Q16842;
A;Experimental source: liver
R;Giordanengo, V.
                                                                                                                                                                                                               밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    beta-galactoside alpha-2,3-sialyltransferase (EC 2.4.99.4) ST3GalA.2 - mous
C;Species: Mus musculus (house mouse)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ś
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, A; Reference number: H00561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    뫄
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: G01021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: beta-galactoside alpha-2,3-sialyltransferase
                                                 170 LQLTRMYPGLQVYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIV 229
                                                                                                                                                                                                                                                                59 YSSVPDGKPL-VREP--CRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 YSSVPDGKPL-VREP--CRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 14.1%;
Similarity 33.3%;
                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                           GQRSTLRVVSHTSVPLLLRNYSHYFQ--KARDTLYMV----WGQGRHMDRVLGGRTYRTL
                                                                                                                                                                                                               FQIVPGENPYRFRDPQQCRRCAVVGNSGNLRGSGYGQEVDSHNFIMRMNQAPTVGFEKDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VYGMVSDSYCREKSHPSVPYHYFEKGR 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LQLTRMYPGLQVYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSRTTHHFMYPESAKNLPANVSFVLVPFKVLDLLWIASALSTGQIRF-----TYAPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GQRSTLRVVSHTSVPLLLRNYSHYFQ--KARDTLYMV----WGQGRHMDRVLGGRTYRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FQIVPGENPYRFRDPHQCRRCAVVGNSGNLRGSGYGQDVDGHNFIMRMNQAPTVGFEQDV
                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                               14.1%; Score 228.5; 34.6%; Pred. No. 1.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---DKEKVQIYNPAFFKYIHDRWTEHHGRYPSTGMLVLFFALHVCDEVN
--DKEKVQIYNPAFFKYIHDRWTEHHGRYPSTGMLVLFFALHVCDEVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24;
                                                                                                                                                                                                                                                                                                                   23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 230; DB 2;
Pred. No. 1.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            March 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GB:U63090; NID:g1773282; PIDN:AAB40389.1; PID:g1773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                   No. 1.8e-12;
smatches 75;
                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82; Indels
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                    Length 350;
                                                                                                                                                                                                                                                                                                                   25;
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                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                              169
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                                                                                                          243
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RESULT 4
CR017

JC8017

beta-galactoside alpha-2,6-sialyltransferase (EC 2.
c;Species: Mus musculus (house mouse)
C;Date: 04-Apr-2004 #sequence_revision 04-Apr-2004
C;Accession: JC8017
R;Takashima, S; Tsuji, S; Tsujimoto, M.
J. Biochem. 134, 287-296, 2003
밁
                                                                                                                                                                               A;Cross-references: UNIPROT:P54751; EMBL:X73523; NID:g402214; C;Superfamily: beta-galactoside alpha-2,3-sialyltransferase C;Keywords: glycosyltransferase
                                                                                                                                                                                                                                                                                                                                                    Eur. J. Biochem. 216, 377-385, 1993
A;Title: Molecular cloning and expression of Gal-beta-1,3GalNAc-alpha-2,3-sialyltransfers
A;Reference number: S36824; MUID:93387288; PMID:8375377
                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Mus musculus (house mouse)
C;Date: 22-Jan-1994 #sequence_revision 13-Mar-1997
C;Accession: S36824
R;Lee, Y.C.; Kurosawa, N.; Hamamoto, T.; Nakaoka, 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ś
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A;Introns: 310/1; 342/3;
C;Keywords: oligosacchar:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Cross-references: DDBJ:AB095093
C;Comment: This enzyme is an oligosaccharide-specific enzyme and a type II transmembrane
cid to galactose of the Gal betal,4 GlcNAc structure through an alpha 2,6-linkage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Comparison of the enzymatic properties A;Reference number: JC8017; PMID: 12966079 A;Accession: JC8017
                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-337 < LEE>
                                                                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: S36824
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A; Residues: 1-524 < TAK>
                                                                                                                                                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          beta-galactoside alpha-2,3-sialyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: ST6GalII
                                                                                                Matches
                                                                                                                 Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        270 GWRPLVPGVPLSQLHPRGLS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
                                              73
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oligosaccharide-specific; sialyl motif; sialyltransferase;
                                                                                             61;
  CRRCAVVGNSGNLKDSSYGPEIDSHDFVLRMNKAPTVGFEADVGSRTTHHLV------
                        CRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRSTLRVVSHTSVPLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VYGMVSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSGFIGILIMMSMCKEVHVYEYIPSVRQTELCH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STGWFTMILALELCEEIVVYGMVSDSYCREKSHPSVPYH--YFE 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANLNLWYKKPDYNLFTPYIQHRRKYPTQPFYILHPKFIWQLWDIIQENTREKIQPNPP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DRV-----LGGRTYRTLLQLTRMYPGLQVYTFTERMMAYCDQIFQDETGKNRRQSGSFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRFNSAPTRGYEKDVGNKTTVRIINSQ----ILANPSHHFIDSALYKDVILVAWDPAPYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSRPTVPG----PLHFSGYSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECV
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                                                                                             Conservative
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                                                                                        12.9%; Score 209.5; DB 2
32.6%; Pred. No. 8.3e-11;
tive 32; Mismatches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.6%; Score 221.5; DB 2; 28.6%; Pred. No. 1.2e-11; tive 38; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                               T.; Nakaoka, T.; Tsuji,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EC 2.4.99.4) - mouse
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                                                                                                                                          Length
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                                                                                                                                                                                                                                        PIDN: CAA51919.1;
                                                                                                29;
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                                                                                           Gaps
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    187
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C;Species: Rattus norvey....
C;Date: 14-May-1998 #sequence_revision
C;Accession: JC6321
R;Zeng, G; Gao, L; Yu, R.K.
Gene 187, 131-134, 1997
Gene 187, 131-137 of the cDNA coding for
Gene 187, 71, 131-134, 1997
A;Title: Cloning of the cDNA coding for rat brain CMP-NeuAc:GD3 alpha2-8 sialyltra
A;Reference number: JC6321; MUID:97225806; PMID:9073076
A;Recession: JC6321
A;Molecule type: mRNA
A;Residues: 1-390 <ZENN>
A;Cross-references: UNIPROT:P97877; GB:U55938
A;Experimental source: brain
C;Comment: This enzyme is one of the sialyltransferases and adds one more alpha-2, C;Superfamily: alpha-N-acetylneuraminate alpha-2,8-sialyltransferase
C;Koywords: glycosyltransferase
F;18-33/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CMP-NeuAc-GM3 alpha2-8 sialyltransferase (EC 2.4.99.-) N;Alternate names: GD3-synthase; GM3-synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-releven
C;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gal-beta-1,3GalNac alpha-2,3-sialyltransferase - chicken
C;Species: Gallus gallus (chicken)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S55675
R;Kurosawa, N.; Hamamoto, T.; Inoue, M.; Tsuji, S.
Biochim. Biophys. Acta 1244, 216-222, 1995
A;Ttle: Molecular cloning and expression of chick Gal-beta-1,3GalNAc alpha-2,3-sialyltr
A;Reference number: S55675; MUID:95284088; PMID:7766661
A;Accession: S55675; MUID:95284088; PMID:7766661
A;Accession: S55675
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-342 < KUR>
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Best Local Similarity
Matches 61; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: UNIPROT:Q11200; GB:X80503; NID:g975654; PIDN:CAA56666.1; PID:g97565: Superfamily: beta-galactoside alpha-2,3-sialyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215 DLRWIVTALTTGTINFTYVPVPRKIKVRKEKVLIYNPSFIKYVYENWLQNHGRYPSTGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 IPGDRDPLQERGTFS------CRRCAVVGNSGNLRQSQYGQDIDSHDFVLRMNRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 VPG---PLHFSGYSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TMILALELCEEIVVYGMVSDSYCREKSHPSVPYHYFE 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVIFALHVCDEVNVYGFGADS----KGH---WHHYWE 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---HYWE 299
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28.1%; Pred. No. 1.
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1.5e-10;
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C;Species: Mus musculus (house mouse)
(;Date: 19-Oct-1995 #sequence_revision 08-Feb-1996
C;Accession: JC4224
R;Yoshida, Y:, KOjima, N:, Tsuji, S.
J. Biochem. 118, 658-664, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;141-185/Region: sialyl signature L
F;280-302/Region: sialyl signature S
F;50,74,119,204,219/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q64692; EMBL:X86000; NID:g2665331; PIDN:CAA59992.1; PID:g122:A;Experimental source: lung
C;Comment: This enzyme exhibits activity specific toward sialylated glycoproteins. This enzyme exhibits activity specific toward sialylated glycoproteins. This eC;Superfamily: alpha-N-acetylneuraminate alpha-2,8-sialyltransferase
C;Superfamily: alpha-N-acetylneuraminate alpha-2,8-sialyltransferase
C;Keywords: glycoprotein; glycosyltransferase; lung; transmembrane protein
F;8-20/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Blochem. 118, 658-664, 1995
A;Title: Molecular cloning and characterization of a third type A;Reference number: JC4224; MUID:96115941; PMID:8690732
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A; Residues: 1-359 < YOS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 LLQLTRMYPGLQVYTFTER-----MMAYCDQIFQ--DETGKNRRQSGSFLSTGWFTMIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 SLLPDVSPILNKRYNICAVVGNSGILTGSQCGQEIDKSDFVFRCNFAPTEAFHKDVGKKT
                                                                                                                                                                                                                                                                                                                                                                                                     59 YSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGABIDSABCVFRMNQAPTVGFBADVGQR 118
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LNVLHNRGALK
                                          EKAVFSRWAKK 289
                                                                                          TLATRECDEIHLYGFW--PFPKDLNGKAVKYHYYD-
                                                                                                                                                                               ILKNKLQVRTAYPSLRLIHAVRGYWLTNKVPI------
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                                                                                                                                                                                                                                                                                                                    STLRVVSHTSVPLL---LRNYS-----HYFQKARDTL----YMVWGQGRHMDRVLGGR 164
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                                                                                                                                    ILALELCEEIVVYGMVSDSYCREKSHPSVPYHYFEKGRLDECQMYLAHEQAPRSAHRFIT
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IS4229 beta-galactoside alpha-2,3-sialyltransferase C;Species: Homo sapiens (man)

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2.4.99

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J. Biol. Chem. 269, 17872-17878, 1994
A;Title: Differential expression of five sialyltransferase genes in human A;Reference number: A54898; MUID:94299495; PMID:8027041
A;Accession: A54898
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-11,'V',13-340 <KIT>
A;Cross references: GB:L29555; NID:g522196; PIDN:AAA36612.1; PID:g522197
C;Genetics:
                                                                                                                                                                                                                                                               polysialyltransferase-1 - Chinese hamster C;Species: Cricetulus griseus (Chinese hamster) C;Species: Cricetulus griseus (Chinese hamster) C;Cpate: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004 C;Accession: S52425 R;Sckhardt, M; Muehlenhoff, M.; Bethe, A.; Koopman, J.; Frosch, M.; Gerardy-Schahn, Nature 373, 715-718, 1995 A;Title: Molecular characterization of eukaryotic polysialyltransferase-1. A;Reference number: S52425; MUID:95157675; PMID:7854457 A;Accession: S52425
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A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-340 <RES>A;Residues: 1-340 <RES>A;Cross-references: UNIPROT:Q11201; GB:L13972; NID:g4102: R;Kitagawa, H.; Paulson, J.C. J. Bill. Chem. 269, 17872-17878, 1994
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C;Accession: 154229; A54898
R;Chang, M.L.; Eddy, R.L.; Sh
Glycobiology 5, 319-325, 1995
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A;Map position: 3q21-3q28
C;Superfamily: beta-galactoside alpha-2,3-sialyltransferase
C;Keywords: glycosyltransferase
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A; Residues: 1-359 < ECK>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 55
                                                                                                                                                                                 ;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
                                                                                            Matches
                                                                                                                                                                               Cross-references: UNIPROT:Q64690; GB:Z46801; NID:g735953; PIDN:CAA86822.1; PID:g73595
Superfamily: alpha-N-acetylneuraminate alpha-2,8-sialyltransferase
                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 YPGLQVYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 LRNYSHYFQKARDTLYMVWGQGRHMD-----RVLGGRTYRTLL------QLTRM 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 CRRCAVVGNSGNLRESSYGPEIDSHDFVLRMNKAPTAGFEADVGTKTTHHLV------
                                    59 YSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 CRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRSTLRVVSHTSVPLL 132
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                                                                                                                Similarity
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      HSLLPEVSPMKNRRFKTCAVVGNSGILLDSGCGKEIDSHNFVIRCNLAPVVEFAADVGTK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DS---KGNWH-----HYWE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---YPESFRELGDNVSMILVPFKTIDLEWVVSAITTGTISHTYIPVPAKIRVKQDKILIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.2%;
                                                                                         12.1%; Score 196.5; DB 2; 27.5%; Pred. No. 1.2e-09; tive 39; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shows, T.B.; Lau, J.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 198.5; DB 2
Pred. No. 7.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GB:L13972; NID:g410225;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60;
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                                                                                                                                   Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51;
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A;Cross-references: UNIPROT:Q64689; GB:X80502; NID:g929684; PIDN:CAA56665.1; C;Superfamily: alpha-N-acetylneuraminate alpha-2,8-sialyltransferase C;Keywords: transmembrane protein
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Gal beta 1,3GalNAc alpha 2,3-sialyltransferase - pig
(;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 13-Sep-1998
C;Accession: A45073
R;Gillespie, W., Kelm, S.; Paulson, J.C.
J. Biol. Chem. 267, 21004-21010, 1992
A;Title: Cloning and expression of the Gal beta 1, 3GalNAc alpha 2,3-sialylt A;Accession: A45073; MUID:93016016; PMID:1383214
A;Accession: A45073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
A45073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA; protein
A;Residues: 1-343 <GII»
A;Note: sequence extracted from NCBI backbone (NCBIN:116168, NCBIP:116169)
C;Superfamily: beta-galactoside alpha-2,3-sialyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                     Matches
301
                                               244
                                                                                            243
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                                                                                                                                                                                                                                         124 VSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQVYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286 TLATRFCDEIHLYGFW--PFPKDLNGKAVKYHYYD----DLKYRYFSNASPHRMPLEFKT
                                                                                                                                                                                                                                                                                                                                   67 PLVRE---PCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRSTLRV 123
                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity 57; Conserv
                                                                                                                                         FTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMVSDSYCREKS
  H----HYWE
                                               HPSVPYHYFE
                                                                                            KKEKILIYHPAFIKYVFDRWLQGHGRYPSTGILSVIFSLHICDEVDLYGFGADS--KGNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYRTLLQLTRMYPGLQV-----YTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTM 218
                                                                                                                                                                                                                                                                                   PLLEKRIVSCRRCAVVGNSGNIKESYYGPQIDSHDFVLRMNKAPTEGFEADVGSKTTHHF
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                                                                                                                                                                                         VYPESFRELAQEVS
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305
                                                                                                                                                                                                                                                                                                                                                                                                                      11.7%;
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                                                                                                                                                                                                                                                                                                                                                                                     36; Mismatches
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Pred. No. 3.6e-09;
                                                                                                                                                                                         -MILVPFKTTDLEWVISATTTGTISHTYVPVPA-KIKV
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 343;
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## RESULT 12

R;YOShida, Y.; Kojima, N.; Kurosawa, N.; Hamamoto, T.; Tsuji, S.
J. Biol. Chem. 270, 14628-14633, 1995
A;Title: Molecular cloning of Siaalpha2,3Galbeta1,4GlcNAc alpha2,8-sialyltransferase
A;Reference number: A56950; MUID:95301555; PMID:7782326
A;Accession: A56950
A;Status: preliminary; not compared with conceptual translation alpha-2,8-sialytransferase III - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 09-Jul-2004
C;Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 09-Jul-2004
C;Accession: A56950
R;Yoshida, Y:; Kojima, N:; Kurosawa, N:; Hamamoto, T:; Tsuji, S:
J. Biol. Chem. 270, 14628-14633, 1995 A; Molecule type: mRNA A; Residues: 1-380 < YOS>

PID:g929685

fron

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S41114

Gal beta 1,4 GlcNAc alpha 2,6-sialyltransferase - chicken

G;Species: Gallus gallus (chicken)

G;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C;Accession: S41114

R;Kurossawa, N.; Kawasaki, M.; Hamamoto, T.; Nakaoka, T.; Lee, Y.C.; Arita, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alpha-2,8-polysialyltransferase - human
(;Species: Homo sapiens (man)
(;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
(;Accession: I59403
R;Nakayama, J:; Fukuda, M.N.; Fredette, B:; Ranscht, B:; Fukuda, M.
Proc. Natl. Acad. Sci. U.S.A. 92, 7031-7035, 1995
A;Title: Expression cloning of a human polysialyltransferase that forms the A;Reference number: I59403; MUID:95350205; PMID:7624364
A;Reference number; translated from GB/EMBL/DDBJ
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-359 <RES>
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Best Local S
Matches 65
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 HSLLPEVSPMKNRRFKTCAVVGNSGILLDSECGKEIDSHNFVIRCNLAPVVEFAADVGTK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       221 ALELCEEIVVYGMVS---DSYCREKSHPSVPYHYFEK 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 LLQLTRMYPGLQVYTFTER-----MMAYCDQIFQ--DETGKNRRQSGSFLSTGWFTMIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    206 NLT----TFNPSILEKYYNNLLTIQDRNNFFLSLKKLDGAILW-----IPAFFFHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 SLLPDVSPIMNKRYNVCAVVGNSGILTGSQCGQEIDKSDFVSRCNFAPTEAFHKDVGRKT 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 TLRVVSHTSVPLLLRNYSHYFQKARDTL------YMVWGQGRHMDRVLGGRTYRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 YSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 SSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 11.6%; Score 188.5; DB 2; Similarity 27.1%; Pred. No. 6.3e-09;
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                                                                                                                                                                                                      EKAVFSRWAKK 289
                                                                                                                                                                                                                                          TLATRFCDEIHLYGFW--PFPKDLNGKAVKYHYYD----DLKYRYFSNASPHRMPLEFKT
                                                                                                                                                                                                                                                                     ILALELCEEIVVYGMVSDSYCREKSHPSVPYHYFEKGRLDECQMYLAHEQAPRSAHRFIT
                                                                                                                                                                                                                                                                                                                                                   TYRTLLQLTRMYPGLQV-----YTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTM 218
                                                                                                                                                                                                                                                                                                                                                                                       SDFITMNPSVVQRAFGGFRNESDREKFVHRLSMLNDSVLWIPAFMVKGGEKHVEWV-NAL
                                                                                                                                                                                                                                                                                                                                                                                                                          STLRVVSHTSVPLL---LRNYS-----HYFQKARDTL----YMVWGQGRHMDRVLGGR 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SATVTRTL----VDFFVEHRGQLKVQLAWPGNIMQHVNRYWKNKHLSPKRLSTGILMYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASAICEEIHLYGFWPFGFDPNTRE----DLPYHYYDK 341
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Pred. No. 4.5e-09;
18; Mismatches 81;
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                                                         FITEKAVFSR 285
                    FNLEKQVWKR
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alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase (EC 2.4.99.3) - chick C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 30-Jun-1995 #sequence_revision 30-Jun-1995 #text_change 09-Jul-2004
C;Accession: A49880
C;Accession: A49880
T; Lee, Y.C.; Nakaoka, T.; Kojima, N.; Tsuji, S.
J. Biol. Chem. 269, 1402-1409, 1994
A;Title: Molecular cloning and expression of GalNAc alpha2,6-sialyltransferase.
A;Reference number: A49880; MUID:94117458; PMID:8288607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q92183; GB:X74946; NID:g453196; PIDN:CAA52902.1; PID:g453197 C;Superfamily: alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase C;Keywords: glycosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eur. J. Biochem. 219, 375-381, 1994
A;Title: Molecular cloning and expression of chick embryo Gal-beta-1,4GlcNAc-alpha-2,6-s)
A;Reference number: S41114; MUID:94139712; PMID:8307003
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                                                                                                                                                                                                                                                                                                                                                                                                              337 CISCAVVGNGGILNNSGMGQEIDSHDYVFRVSGAVIKGYEKDVGTKTSFYGFTAYSLVSS
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l Similarity 25.2%;
63; Conservative 3
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LLLTALHLCDRVSAYGYITE---
                                                               FTMILALELCEEIVVYGMVSDSYCREKSHPSVPYHYFEKGRLDECQMYLAHEQAPRSAHR
                                                                                                                                   FLNYYGRRPRERFDEDFTMNKYLVAHPDFL---RYLKVRFLKSKNLOKPYWRLYRPTTGA
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                                                                                                                                                                                                   -YTFTERMMAYCDQIFQDETGKNRRQSGSFL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 178; DB 2; ; Pred. No. 9.3e-08; 37; Mismatches 80
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Search completed: December 10, 2004, 18:25:57 Job time : 41 secs

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             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match
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1. /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2. /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3. /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4. /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6. /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Gapop 10.0 , Gapext
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1626
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           GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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  US-09-390-360B-75
US-09-334-601-13
US-09-621-976-3915
US-08-446-875-16
US-08-503-133A-2
US-08-503-133A-2
US-08-957-775A-2
US-08-957-748-2
US-08-102-3856-2
US-08-626-994A-3
US-08-626-994A-3
US-08-626-994A-1
US-08-626-994A-1
US-08-636-3678-6
US-09-143-438-6
US-09-143-438-8
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Sequence 75, Appl
Sequence 13, Appl
Sequence 16, Appl
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
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Sequence 6, Appli
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Sequence 10, Appli
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Sequence 21, Appli
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Sequence 4, Appli
Sequence 20, Appli
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Sequence 4, Appli
Sequence 20, Appli
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181 181

241 EKSHPSVPYHYFEKGRLDECQMYLAHEQAPRSAHRFITEKAVFSRWAKKRPIVFAHPSWR 300

240

240 180

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180

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| Query Match Best Local Matches 30 Qy 1 Db 1                                   | RESULT 1  US-09-599-360B- Sequence 75, Patent No. 65 GENERAL INFOR APPLICANT: APPLICANT: APPLICANT: TITLE OF INV FILE REFEREN CURRENT APPL CURRENT APPL CURRENT FILING PRIOR FILING PRIOR FILING PRIOR FILING PRIOR FILING PRIOR APPLIC FEATURE: FEATURE: INAME/KEY: US-09-599-360B-   |            | 28 16<br>29 16<br>30 166.<br>31 166.<br>32 166.<br>32 163.<br>34 163.<br>35 15.<br>37 148.<br>39 145.<br>40 14.<br>41 14.<br>42 14.  |
|---|--|------------|--|
| ່ ວິທີ  | 08-75 6548633 FORMATION: Dumas Mil: Dumas Mil: Bouguele: Jobert, INVENTION: RENCE: GENSS PPLICATION ULICATION NUT ING DATE: 1 LICATION NUT ING DATE: 1 SIGNAL: Homo Sapi SIGNAL: SIGNAL: SIGNAL: SIGNAL: STORMATON OSAPI SIGNAL: SIGNAL: SIGNAL: SIGNAL: SOME SAPI SOME SAPI SIGNAL: SIGNAL |            | 168 10.3<br>168 10.3<br>16.5 10.3<br>15.5 10.2<br>17.5 9.7<br>17.5 9.7<br>17.43 8.8<br>17.43 8.8<br>17.43 8.8<br>17.43 8.8<br>17.43 8.8<br>17.43 8.8<br>17.43 8.8  |
| 100.0%;<br>100.0%;<br>ative<br>ILCSVVFSA<br>                                  | ation US/095993 : ilne Edwards, J leret, L S. Complementary NSET.050CP3 N NUMBER: US/09 E: 2000-06-21 NUMBER: 60/113, 1998-12-2 1999-06-25 NUMBER: 60/441, 1999-06-25 NUMBER: 09/469, 1999-12-21 mm  |            | 744<br>7406<br>7467<br>90<br>340<br>90<br>340<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>332<br>90<br>90<br>90<br>90<br>90<br>90<br>90<br>90<br>90<br>90<br>90<br>90<br>90 |
| Score 1626; DB 4; Pred. No. 3.4e-170; 0; Mismatches 0; NYILLCCWAGLPLCLATCLDHH | US/09599360B  idwards, J.B. L.  L.  L.  L.  100-06-21  12-22  10-25-141,032  10-21  12-21  | ALIGNMENTS | US-08-446-777-4 US-08-446-777-8 US-09-344-601-22 US-09-334-601-24 US-10-140-002-462 US-08-361-304A-2 US-08-361-304A-2 US-08-34-601-25 US-09-334-601-25 US-09-334-601-25 US-09-334-601-25 US-09-334-601-25 US-09-34-601-25 US-09-34-601-25 US-09-34-601-25 US-08-406-875-12 US-08-406-875-12 US-08-406-875-12 US-08-346-875-12 US-08-346-875-12 US-08-346-875-12 US-08-346-875-12 US-08-346-875-12 US-08-102-385G-12 US-09-334-601-8 US-09-334-601-8 US-09-334-601-8 US-09-334-601-8 US-09-334-601-8 US-08-102-385G-12 US-08-102-385G-12  |
| Length 302; Indels 0; Gaps 0 FPTGSRPTVPGPLHFSGYS 60                           | ins with Signal Peptides   |            | Sequence 4, Appli<br>Sequence 6, Appli<br>Sequence 22, Appli<br>Sequence 24, Appl<br>Sequence 24, Appl<br>Sequence 24, Appli<br>Sequence 2, Appli<br>Sequence 23, Appli<br>Sequence 26, Appli<br>Sequence 27, Appli<br>Sequence 12, Appli<br>Sequence 12, Appli<br>Sequence 12, Appli<br>Sequence 12, Appli<br>Sequence 12, Appli<br>Sequence 13, Appli<br>Sequence 12, Appli<br>Sequence 13, Appli<br>Sequence 15, Appli  |

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CURRENT APPLICATION NUMBER: US/09/334,601
CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 94
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 336
TYPE: PRT
ORGANISM: Homo sapiens
US-09-334-601-13
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                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
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Matches
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                                                                                                       NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 3915
                                                                                                                                                                                                                                                                                                    Sequence 3915, Application US/09621976 Patent No. 6639063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 47.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kapitonov, Dmitri
APPLICANT: Yu, Robert
TITLE OF INVENTION: NOVEL SIALYLTRANSFERASES
                                                                                                                                                         FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: VCUIP-6
                                                   TYPE: PRT ORGANISM: Homo sapiens
NAME/KEY: SIGNAL LOCATION: -18..-1
                                     FEATURE:
                                                                                       ENGTH: 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 MNOAPTVGFEADVGQRSTLRVVSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                               282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 TGSRPTVP-GPLHFSGYSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGABIDSABCVFR 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GQVYNNLHLLSQVLPRLKAFMITRHKMLQFDELFKQETGKDRKISNTWLSTGWFTMTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                               VFKNWARTFNIHFFQPDWKPE 323
                                                                                                                                                                                                                                                                                                                                                                                                                                             VFSRWAKKRPIVFAHPSWRTE 302
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; OTHER INFORMATION: US-09-621-976-3915
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, MOLECULE TYPE: protein US-08-446-875-16
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Best Local Similarity
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                                                                                                                                    APPLICATION NUMBER: US/08/446,875
FILING DATE: July 12, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/102,385
FILING DATE: AUGUST 4, 1993
ATTORNEY/AGRAY INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 111-197
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 788-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                    TELEFAX: (310) 277-1297 INFORMATION FOR SEQ ID NO:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Poms, Smith, Lande & Rose
STREET: 2029 Century Park East, Suite 3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Burlingame, Alma L.
APPLICANT: Medzihradszky, Katalin
APPLICANT: Medzihradszky, Katalin
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Identification and Synthesis of Sialyltransferases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                    TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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                                                                  340 amino acids
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Livingston, Brian Duane
Gillespie, William
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Pred. No. 1.7e-46;
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US-08-503-133A-2
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Matches
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                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION UMMERR: US/08/503,133A
FILING DATE: 17-JULY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/04289
FILING DATE: 22-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HANSON, NO. 5747326man D.
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                         TELEFAX: (212) 838-3884 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: BC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PS/
OPERATING SYSTEM:
                                                                                           Local Similarity
                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                             TELEPHONE:
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                                                                                                                                                                                                                      LENGTH:
 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 YPGLQVYTFTERWMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 CRRCAVVGNSGNLRESSYGPEIDSHDFVLRWNKAPTAGFEADVGTKTTHHLV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 DSYCREKSHPSVPYHYFE 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 LRNYSHYFQKARDTLYMVWGQGRHMD-----RVLGGRTYRTLL------QLTRM 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 CRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRSTLRVVSHTSVPLL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity 27.8
55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1002
                                                                                                                                                                                    amino acid
GY: linear
HSLLPEVSPMKNRRFKTCAVVGNSGILLDSGCGKEIDSHNFVIRCNLAPVVEFAADVGTK 184
                                  YSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQR 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DS--KGNWH-----HYWE 302
                                                                                                                                                                                                                    359 amino acids
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                                                                          Conservative
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Nakayama, Jun; Eckhardt, Matthias
MENTION: Isolated Polysialyl Transferases,
MENTION: Nucleic Acid Molecules Coding Therefor, Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PS/2
                                                                                                                                                                                                                                                                                               (212)
                                                                                                                                                               protein
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                                                                                                                                                                                                                                                                                           688-9200
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                                                                                       12.1%; Score 196.5; DB 1
27.5%; Pred. No. 6.4e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PC-DOS
                                                                      39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32;
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pred. No. 3.6e-13;
2; Mismatches 60;
                                                                        Mismatches
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                                                                                                      DB 1;
                                                                        98;
                                                                      Indels
                                                                                                          Length
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                                                                                                                      ; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-576-775A-2
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                                           Matches
                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                        TELEFAX: (212) 838-388
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
PRIOR APPLICATION DATA:
08/503,133
                                                                                                                                                                                                                                                                                                                                               FILING DATE: 22-December-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5849904man D.
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gerardy-Schahn, Rita; Fukuda, Minoru;
APPLICANT: Nakayama, Jun; Eckhardt, Matthias
TITLE OF INVENTION: Isolated Pollysiallyl Transferases,
TITLE OF INVENTION: Nucleic Acid Molecules Coding Therefor, Methods of
TITLE OF INVENTION: Production and Use
                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: BO TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/50 FILING DATE: 17-July-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Wordperfec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 TYRTLLQLTRMYPGLQV-----YTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTM 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 SDFITMNPSVVQRAFGGFRNESDRAKFVHRLSMLNDSVLWIPAFMVKGGEKHVEWV-NAL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 ILKNKLKVRTAYPSLRLIHAVRGYWLTNKVPI-----
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    59 YSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQR 118
                                                                                                                                                                                amino acid
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                                                                                                                                                                                                       359 amino acids
                                                                                                                                                                                                                                                               (212) 838-3884
                                           Conservative
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                                                                                                                                                                                                                                                                                      (212)
                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-December-1995
                                         12.1%; Score 196.5; DB 2
27.5%; Pred. No. 6.4e-13;
ative 39; Mismatches 98
                                                                                                                                                                                                                                                                                    688-9200
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                                                                                 DB 2;
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                                           Indels
                                           45;
                                           Gaps
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125 HSLLPEVSÞMKNRRFKTCAVVGNSGILLDSGCGKEIDSHNFVIRCNLAPVVEFAADVGTK 184

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US-08-972-498-2
                                                                                                                   ; MOLECULE TYPE: protein US-08-972-498-2
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; Patent No. 5959078
; GENERAL INFORMATION:
APPLICANT: Gerardy
APPLICANT: Nakayam
; APPLICANT: NAKAYAM
                                          Matches
                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/EP94/0428
FILING DATE: 22-December-1994
ATTORNEY/AGENT INFORMATION:
NAME: HANSON, NO. 5959078man D.
REGISTRATION NUMBER: 30.946
REFERENCE/DOCKET NUMBER: BOER 105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION UNMERE: 08/576,775
FILING DATE: 21-December-1995
APPLICATION NUMBER: 08/503,133
FILING DATE: 17-July-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DC
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: Felfe & Lynch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gerardy-Schahn, Rita; Fukuda, Minoru;
APPLICANT: Nakayama, Jun; Eckhardt, Matthias
TITLE OF INVENTION: Isolated Polystalyl Transferases,
TITLE OF INVENTION: Nucleic Acid Molecules Coding Therefor, Methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FITLE OF INVENTION:
                                                                                                                                            TYPE: amino acids
TOPOLOGY: lines~
LECUTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 SDFITMNPSVVQRAFGGFRNESDRAKFVHRLSMLNDSVLWIPAFMVKGGEKHVEWV-NAL 243
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59 YSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQR 118
                                          69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYRTLLQLTRMYPGLQV-----YTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTM 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STIRVVSHTSVPLL---LRNYS-----HYFQKARDTL----YMVWGQGRHMDRVLGGR 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08972498
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                                                                                                                                                                                                                                                                  (212)
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                              2) 688-9200
838-3884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PC-DOS
                                       12.1%; Score 196.5; DB 2; 27.5%; Pred. No. 6.4e-13; tive 39; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                            PCT/EP94/04289
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                                            Indels
                                                                               Length 359;
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                                                                                                                                        ; MOLECULE TYPE: protein US-08-899-545-2
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                                                                    Matches
                                                                                                      Query Match
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MEDIUM TYPE: Diskette, 3.5 inch, 36.

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/899,545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
ATTORNEY AGENT INFORMATION:
NAME: Hanson, No. 6020201man
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                TELEFAX: (212) 838-3884 INFORMATION FOR SEQ ID NO: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gerardy-Schahn, Rita; Fukuda, Minoru;
APPLICANT: Nakayama, Jun; Eckhardt, Matthias
TITLE OF INVENTION: Isolated Polysialyl Transferases,
TITLE OF INVENTION: Nucleic Acid Molecules Coding Therefor,
TITLE OF INVENTION: Production and Use
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                         LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York City
                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                     TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              286
125 HSLLPEVSPMKNRRFKTCAVVGNSGILLDSGCGKEIDSHNFVIRCNLAPVVEFAADVGTK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10022
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                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STLRVVSHTSVPLL---LRNYS-----HYFQKARDTL----YMVWGQGRHMDRVLGGR 164
                      YSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGABIDSAECVFRMVQAPTVGFEADVGQR 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Felfe & Lynch
805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                       (212) 688-9200
                                                                      12.1%; Score 196.5; DB 3
27.5%; Pred. No. 6.4e-13;
tive 39; Mismatches 98
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                                                                                                          DB 3;
                                                                        98;
                                                                                                        Length 359;
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                                                                          Gaps
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                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-875-2
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US-08-446-875-2
                                                                                   Matches
                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                   TELEFAX: (310) 277-1297 INFORMATION FOR SEQ ID NO: : SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOTTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/446,875
FILING DATE: July 12, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tent No.
                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 111-197
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 788-5000
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/102,385
FILING DATE: August 4, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Compositions and Methods for TITLE OF INVENTION: Identification and Synthesis
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                                                                               / Match 11.7%; Score 191; DB 2; Length 343;
Local Similarity 30.0%; Pred. No. 2.4e-12;
nes 57; Conservative 36; Mismatches 77; Indels
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                                                                                                                                                                                                                                              LENGTH: 343 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 ILKNKLKVRTAYPSLRLIHAVRGYWLTNKVPI----
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133 PLLEKRLVSCRRCAVVGNSGNLKESYYGPQIDSHDFVLRMNKAPTEGFEADVGSKTTHHF 192
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5. 5858751
                                67 PLVRE---PCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRSTLRV 123
                                                                                                                                                                                                                        amino acid
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2029 Century Park East, Suite 3800
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Gillespie, William
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Trian Duane
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                                                                                                                                                                                                                                                                                                                                                                                       29,421
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of Sialyltransferases
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                                                                                 Gaps
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                                                                                                                                 Matches
                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 04-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION UNMBER: 29,421
REFERENCE/DOCKET NUMBER: 97-0
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                      TELEPHONE: (310)788-5000
TELEFAX: (310) 277-1297
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Medzihradszky, Katalin
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Identification and Synthesis of Sialyltransferases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: CA
                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0 FILING DATE: 04-AUG-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                      LENGTH: 343 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 FTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMVSDSYCREKS 243
124 VSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQVYT 183
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                                                                                                                                 1 Similarity 57; Conserv
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                                                       PLVRE---PCRSCAVVSSSGQMLGSGLGABIDSAECVFRMNQAPTVGFEADVGQRSTLRV 123
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Livingston, Brian Duane
Gillespie, William
                                                                                                                                   Conservative
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                                                                                                                                                                                                                             protein
                                                                                                                               11.7%; Score 191; DB 2; 1 30.0%; Pred. No. 2.4e-12; ative 36; Mismatches 77;
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                                                                                                                                                                                                                                                                                                                                                                                                          97-062
                                                                                                                                                                     Length 343;
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US-08-626-994A-3
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                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (703) 716-1180
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Shuich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Shuichi
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 33,094
REFERENCE/DOCKET NUMBER: PI-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: JP 77469/1995
FILING DATE: APRIL 3, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/
FILING DATE: April 3, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: 1.44 diskette COMPUTER: IBM PC compatible OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Word Perfect 5.1+ (ASCII)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
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                                                                      212 SATVTRTL----VDFFVEHRGQLKVQLAWPGNIMQHVNRYWKNKHLSPKRLSTGTLMYTL
                                                                                                          169 LLQLTRMYPGLQVYTFTER-----MMAYCDQIFQ--DETGKNRRQSGSFLSTGWFTMIL 220
                                                                                                                                                   165 NLT----TENPSILEKYYNNLLTIQDRNNFFLSLKKLDGAILW------IPAFFFHT
                                                                                                                                                                                     120 TLRVVSHTSVPLLLRNYSHYFQKARDTL------YMVWGQGRHMDRVLGGRTYRT 168
                                                                                                                                                                                                                              105 SLLPDVSPIMNKRYNVCÄVVGNSGILTGSQCGQEIDKSDFVSRCNFÄPTEAFHKDVGRKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 FTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMVSDSYCREKS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193 VYPESFRELAQEVS------MILVPFKTTDLEWVISATTTGTISHTYVPVPA-KIKV
                                 221 ALELCEEIVVYGMVS---DSYCREKSHPSVPYHYFEK 254
                                                                                                                                                                                                                                                                                                     65;
                                                                                                                                                                                                                                                               60 SSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMQAPTVGFEADVGQRS 119
                                                                                                                                                                                                                                                                                                                       h 11.7%;
Similarity 30.0%;
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ASAICEEIHLYGFWPFGFDPNTRE----DLPYHYYDK 300
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1941 Roland Clarke Place
                                                                                                                                                                                                                                                                                                                                                                                                                                                         339 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (703) 716-1191
(703) 716-1191
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Sia' 2,3Gala 1,4GlcNAc ' 2,8-
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                                                                                                                                                                                                                                                                                                                                                                                                                   relevant
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                                                                                                                                                                                                                                                                                                     28;
                                                                                                                                                                                                                                                                                                 Score 190.5; DB 1;
Pred. No. 2.7e-12;
Pred. No. 2.7e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P14595
                                                                                                                                                                                                                                                                                                     Indels 43;
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US-08-626-994A-1
; Sequence 1, Application US/08626994A
; Patent No. 5798244
; GENERAL INFORMATION:
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                                                                            RESULT 13
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Patent No. 6017743
GENERAL INFORMATION:
APPLICANT: Shuichi TSUJI et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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APPLICATION NUMBER: 08/626,994
FILING DATE: April 3, 1996
APPLICATION NUMBER: JP 77469/1995
FILING DATE: April 3, 1995
ATTORNEY/AGENT INFORMATION:
NAME: ATTOID TURK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION: Sia 2,3Gala 1,4G
TITLE OF INVENTION: SIALYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 716-1191
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ADDRESSEE: Greenblum & Bernstein, P.L.C.
STREET: 1941 Roland Clarke Place
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (703)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 339 amino acids
TYPE: amino acid
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OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1+ (ASCII)
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                                                                                                                                                                   221 ALELCEEIVVYGMVS---DSYCREKSHPSVPYHYFEK 254
                                                                                                                                                                                                                                              169 LLQLTRMYPGLQVYTFTER-----MMAYCDQIFQ--DETGKNRRQSGSFLSTGWFTMIL
                                                                                                                                                                                                                                                                                     165 NLT----TENPSILEKYYNNLLTIQDRNNFFLSLKKLDGAILW------IPAFFFHT
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                                                                                                                                  268 ASAICEEIHLYGFWPFGFDPNTRE----DLPYHYYDK 300
                                                                                                                                                                                                           212 SATVTRTL----VDFFVEHRGQLKVQLAWPGNIMQHVNRYWKNKHLSPKRLSTGILMYTL
                                                                                                                                                                                                                                                                                                                        120 TLRVVSHTSVPLLLRNYSHYFQKARDTL-----YMVWGQGRHMDRVLGGRTYRT
                                                                                                                                                                                                                                                                                                                                                                                                  60 SSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRS
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Y: U.S.A.
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716-3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       11.7%; Score 190.5; DB 3; 30.0%; Pred. No. 2.7e-12; ative 28; Mismatches 81;
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                                                                                                                                                                                                                                                                                           211
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APPLICANT: Shuichi TITLE OF INVENTION: TITLE OF INVENTION:

Shuichi TSUJI et al.
VENTION: Sia' 2,3Gala 1,4G1cNAc '
VENTION: SIALYLTRANSFERASE

NUMBER OF SEQUENCES

COUNTRY:

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                                                                                                                                                                       Sequence 1, Application US/08957742
Patent No. 6017743
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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REFERENCE/DOCKET NUMBER: P145
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 716-1191
TELEPAX: (703) 716-1180
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local S
                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenblum & Bernstein, P.L.C
STREET: 1941 Roland Clarke Place
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PAPPLICATION NUMBER: JP 77469/1995
PILING DATE: April 3, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold Turk
                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenblum & Bernstein,
STREET: 1941 Roland Clarke Place
                                                                                                                                                         APPLICANT:
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: 1.44 di
                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 11.7%; Score 190.5; DB Local Similarity 30.0%; Pred. No. 3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: not
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FILING DATE: April 3, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
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                                                                                                                                                                                                                                                                                                                293
                                                                                                                                                                                                                                                                                                                                                                                         237 SATVIRTL----VDFFVEHRGQLKVQLAWPGNIMQHVNRYWKNKHLSPKRLSTGILMYTL
                                                                                                                                                                                                                                                                                                                                                                                                                           169 LLQLTRMYPGLQVYTFTER-----MMAYCDQIFQ--DETGKNRRQSGSFLSTGWFTMIL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 NLT----TFNPSILEKYYNNLLTIQDRNNFFLSLKKLDGAILW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 TLRVVSHTSVPLLLRNYSHYFQKARDTL------YMVWGQGRHMDRVLGGRTYRT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 SLLPDVSPIMNKRYNVCAVVGNSGILTGSQCGQEIDKSDFVSRCNFAPTEAFHKDVGRKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 SSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRS 119
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: Virginia
RY: U.S.A.
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                      Reston
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Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    364 amino acids
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                                                                                                                                                         Shuichi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              not relevant
                                                                                                              TSUJI et al.
Sia' 2,3Gala 1,4GlcNAc '
SIALYLTRANSFERASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-957-742-1
                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08666367B Patent No. 5854042 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 11.7%; Score 190.5; DB 3; Best Local Similarity 30.0%; Pred. No. 3e-12; Matches 65; Conservative 28; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (703) 716-1180 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth,
STREET: 805 Fifteenth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: AIIIII 33, U94
REGISTATION NUMBER: 91.
REFERENCE DOCKET NUMBER: P1.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 116-1191
                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/626,994
FILING DATE: April 3, 1996
APPLICATION NUMBER: JP 77469/1995
FILING DATE: April 3, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold Turk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Word Perfect 5.1+ (ASCII) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 di
                                                                                              COUNTRY: U.
ZIP: 20005
                COMPUTER: IBM Con
OPERATING SYSTEM:
                                                                                                                                                        CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Word Perfect 5.1+
  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 ALELCEEIVVYGMVS---DSYCREKSHPSVPYHYFEK 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 SATVTRTL----VDFFVEHRGQLKVQLAWPGNIMQHVNRYWKNKHLSPKRLSTGILMYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 LLQLTRMYPGLQVYTFTER-----MMAYCDQIFQ--DETGKNRRQSGSFLSTGWFTMIL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 TLRVVSHTSVPLLLRNYSHYFQKARDTL------YMVWGQGRHMDRVLGGRTYRT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 SLLPDVSPIMNKRYNVCAVVGNSGILTGSQCGQEIDKSDFVSRCNFAPTEAFHKDVGRKT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 SSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRS 119
                                                                                                                                       Ð.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NLT----TFNPSILEKYYNNLLTIQDRNNFFLSLKKLDGAILW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASAICEEIHLYGFWPFGFDPNTRE----DLPYHYYDK 325
                                                                                                                  U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       364 amino acids
                  PE: Diskette, 3.1
IBM Compatible
SYSTEM: MS-DOS
                                                                                                                                                                                                                                                            Shuichi TSUJI et al.
VENTION: NOVEL SUGAR-CHAIN SYNTHETASE AND PROCESS FOR
VENTION: PRODUCING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U.S.A.
Wordperfect 5.1
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Street, N.W., #700
                                                        3.5 inch,
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                                                            1.44 mb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.9%; Score 178; DB 2; Length 355; Best Local Similarity 25.2%; Pred. No. 6.8e-11; Matches 63; Conservative 37; Mismatches 80; Indels 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/666,367B
FILING DATE: August 19, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WALTER M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                           186 LONLGHKGFKKI------POGKHI-----RYIHFLEAVRDYEWLKALLLDKDIRKG 230
                                                                                                                                                                                                                                                               133 LRNYSHY-FQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQV------ 181
                                                                                                            216 FIMILALELCEEIVVYGMVSDSYCREKSHPSVPYHYFEKGRLDECQMYLAHEQAPRSAHR 275
                                                                                                                                                231 FLNYYGRRPRERFDEDFTMNKYLVAHPDFL---RYLKNRFLKSKNLQKPYWRLYRPTTGA 287
                                                                                                                                                                                                                                                                                                       333 FNLEKQVWKR 342
                                                                          276 FITEKAVESR 285
                                                                                                                                                                                                                                                                                                                                        73 CRSCAVVSSSGOMLGSGLGAEIDSAECVFRWNQAPTVGFEADVGQRSTLRVVSHTSVPLL 132
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Search completed: December 21, 2004, 22:44:59 Job time : 27 secs

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Result
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Maximum
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM protein - protein search, using sw
                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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716.5
716.5
714.5
713.5
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1622
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seq length: 2000000000
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Match
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Gapop 10.0 , Gapext
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1626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 December 21, 2004, 22:13:05; Search time 77 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKAPGRLVLIILCSVVFSAV......FSRWAKKRPIVFAHPSWRTE 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
                                                                                                                                                                                                                         Length
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/cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
   В
US-09-978-360A-407
US-10-311-664-75
US-09-895-298-120
US-09-895-298-120
US-10-262-511-184
US-10-844-874-20
US-09-833-245-1914
US-09-833-245-1914
US-10-188-186-22
US-10-118-186-24
US-10-1188-186-24
US-10-1188-186-24
US-10-188-186-24
US-10-188-186-24
US-10-188-186-24
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1403.457 Million cell updates/sec
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                                       Sequence 407, App
Sequence 75, Appl
Sequence 66, Appl
Sequence 120, App
Sequence 104, App
Sequence 20, Appl
Sequence 1914, App
Sequence 1915, App
Sequence 22, Appl
Sequence 23, Appl
Sequence 24, Appl
                                                                                                                                                                                                                         Description
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| 45          | 44             | 43            | 42             | 41             | 40            | 39            | 38            | 37             | 36           | 35            | 34            | 33            | 32            | 31            | 30            | 29            | 28           | 27            | 26             | 25                | 24             | 23           | 22             | 21           | 20       | 19           | 18          | 17    | 16           | 15           | 14                |
|-------------|----------------|---------------|----------------|----------------|---------------|---------------|---------------|----------------|--------------|---------------|---------------|---------------|---------------|---------------|---------------|---------------|--------------|---------------|----------------|-------------------|----------------|--------------|----------------|--------------|----------|--------------|-------------|-------|--------------|--------------|-------------------|
| 537         | 537            | 537           | 537            | 537            | 537           | 537           | 537           | 537            | 537          | 537           | 537           | 537           | 537           | 537           | 537           | 537           | 537          | 537           | 537            | 537               | 537            | 537          | 537            | 537          | 537      | 537          | 537         | 537   | 1.3          | 636.5        | 1.3               |
|             | ۳.             | ω.            | ۳              | ω.             | ω.            | ω             | ω.            | ω.             | 33.0         | ω.            | ω.            | ω.            | Ψ             | ü             | Ψ             | ۳             | ·            | ۳             | ۳              | ·                 | ·              | 'n           | Ψ              | Ψ            | ·        | ·            | Ψ           | ω.    | 9            | ۰.           | 9                 |
| 299         | 299            | 299           | 299            | 299            | 299           | 299           | 299           | 299            | 299          | 299           | 299           | 299           | 299           | 299           | 299           | 299           | 299          | 299           | 299            | 299               | 299            | 299          | 299            | 299          | 299      | 299          | 299         | 299   | 336          | 336          | 336               |
| 14          | 14             | 14            | 14             | 14             | 14            | 14            | 14            | 14             | 14           | 14            | 14            | 14            | 14            | 14            | 14            | 14            | 14           | 14            | 14             | 14                | 14             | 14           | 14             | 14           | 14       | 14           | 13          | 10    | 16           | 14           | 14                |
| -176-747-20 | -10-176-492-20 | -10-176-488-2 | -10-175-743-20 | -10-175-740-20 | -10-175-739-2 | -10-174-588-2 | -10-174-582-2 | -10-174-579-20 | 0-174-572-20 | -10-173-700-2 | -10-180-557-2 | -10-180-552-2 | -10-176-913-2 | -10-176-757-2 | -10-176-482-2 | -10-175-752-2 | -10-175-738- | -10-173-706-2 | -10-176-915-20 | US-10-176-914-206 | -10-176-749-20 | -10-176-483- | -10-174-581-20 | -10-175-737- | 6-758-20 | -10-174-590- | 86-20       | 74-   | -10-398-038- | -10-288-252- | 0-094-            |
| æ           | equence 206,   | e 206,        | e 206,         | e 206,         | e 206,        | e 206,        | e 206,        | e 206,         | e 206,       | e 206,        | e 206,        | e 206,        | 206,          | e 206,        | æ             | e 206,        | e 206,       | e 206         | e 206          | e 206             | æ              | e 206        | e 206          | e 206        | e 206    | e 206        | equence 206 | e 56, | e 11,        | e 11,        | Sequence 2441, Ap |

## ALIGNMENTS

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PRIOR APPLICATION NUMBER: US 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-12-17
PRIOR PILING DATE: 1997-12-17
PRIOR PILING DATE: 1998-02-09
PRIOR PILING DATE: 1998-02-09
PRIOR PILING DATE: 1998-04-13
PRIOR PILING DATE: 1998-04-13
PRIOR FILING DATE: 1998-04-13
PRIOR PILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: US 60/096,116
PRIOR APPLICATION NUMBER: US 60/099,273
PRIOR APPLICATION NUMBER: US 09/191,997
PRIOR APPLICATION NUMBER: US 09/191,997
PRIOR APPLICATION NUMBER: US 09/215,435
PRIOR APPLICATION NUMBER: US 09/215,435
PRIOR APPLICATION NUMBER: US 09/215,435
PRIOR APPLICATION NUMBER: PCT/IB98/02122
PRIOR APPLICATION NUMBER: PCT/IB98/02122
PRIOR APPLICATION NUMBER: PCT/IB98/02122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste Dumas Milne
APPLICANT: Duclert, Aymeric
APPLICANT: Dougueleret, Lydie
APPLICANT: Jobert, Severin
APPLICANT: Clusel, Catherine
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
FILE REFERENCE: 56.US4.CIP
CURRENT APPLICATION NUMBER: US/09/978,360A
CURRENT FILING DATE: 2001-10-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 407, Application US/09978360A Publication No. US20040110939A1
                                                                     PRIOR FILING DATE: 1999-02-09
                                                                                                      PRIOR APPLICATION NUMBER: US 09/247,155
Application data removed - See File Wrapper or PALM NOS: 810
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Sequence Sequence

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APPLICANT: Jobert, S.
TITIE OF INVENTION: Complementary DNA's Encoding Proteins with Signal TITIE OF INVENTION: Peptides
FILE REFERENCE: GENSET.050CP3
CURRENT PILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US/10/315,664
CURRENT FILING DATE: 2000-06-21
PRIOR FILING DATE: 2000-06-21
PRIOR FILING DATE: 2000-06-21
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113,686
PRIOR APPLICATION NUMBER: 60/141,032
PRIOR APPLICATION NUMBER: 60/141,032
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patent.pm
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US-10-315-664-75
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; LOCATION: -18..-1
US-09-978-360A-407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 1626; DB 11; Best Local Similarity 100.0%; Pred. No. 2.4e-160; Matches 302; Conservative 0: Mismatchec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patent
SEQ ID NO 407
LENGTH: 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 75, Application US/10315664
Publication No. US20030203377A1
GENERAL INFORMATION:
                                                                                                                                                                       SEQ ID NO 75
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Bougueleret, L. APPLICANT: Jobert, S.
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                                                                FEATURE:
NAME/KEY: SIGNAL
LOCATION: -18..-
                                                                                                                   TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                       ENGTH:
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 100.0%;
   Score
Pred.
 1626; DB 14;
No. 2.4e-160;
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Sequence 66, Application US/09895298

Publication No. US20030078405A1

Publication No. US20030078405A1

GENERAL INFORMATION:
APPLICANT: ROSen et al.
APPLICANT: ROSen et al.
FILE REFERENCE: PZ035P1

CURRENT APPLICATION NUMBER: US/09/895,298

CURRENT FILING DATE: 2001-07-02

PRIOR APPLICATION NUMBER: 09/591,16

PRIOR APPLICATION NUMBER: PCT/US9/29950

PRIOR APPLICATION NUMBER: PCT/US9/29950

PRIOR APPLICATION NUMBER: 60/113,006

PRIOR APPLICATION NUMBER: 60/113,006

PRIOR APPLICATION NUMBER: 60/113,006

PRIOR APPLICATION NUMBER: 1998-12-16

PRIOR APPLICATION NUMBER: 60/113,006

PRIOR APPLICATION NUMBER: 60/113,006
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                                                                                                                                                                                                                                                 LENGTH: 302
TYPE: PRT
CORGANISM: Homo sapiens
FEATURE:
INDEXESTRE:
LOCATION: (237)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-895-298-66
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                                                                                                                                                                                        Matches
                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/112,809
PRIOR FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 231
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Pred. No. 6.2e-160;
0; Mismatches 1;
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APPLICATION NUMBER: 09/112,809
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 09/591,16
PRIOR APPLICATION NUMBER: 09/591,16
PRIOR APPLICATION NUMBER: PCT/US99/29950
PRIOR APPLICATION NUMBER: 60/113,006
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 60/112,809
PRIOR APPLICATION NUMBER: 50/112,809
PRIOR APPLICATION NUMBER: 50/112,809
PRIOR FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 231
SOFTWARE: PATEENTIN Ver. 2.0
SEQ ID NO 120
LENGTH: 345
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
, NAME/KEY: SITE
, LOCATION: (280)
, LOCATION: (280)
, OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-895-298-120
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US-09-895-298-120
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Best Local Similarity 99.7%;
Matches 301; Conservative
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344
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                                       301
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                                     TE 302
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TE 345
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b. US20030078405A1
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Pred. No. 7.5e-160;
0; Mismatches 1;
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RESULT 5

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Gaps

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-184
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PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR APPLICATION NUMBER: 60/381,038
                   Query Match
Best Local Similarity
                                                                                                                                              Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 184
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Matches
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APPLICANT: Smithson, Glennda
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
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                                                                                                                                                                                                                            PRIOR FILING DATE: 2001-10-05
                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/373,260
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PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
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PRIOR APPLICATION NUMBER: 60/373,826
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                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/327,435
 218;
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Pena, Carol E. A.
Shenoy, Suresh G.
Shimkets, Richard A.
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Peyman, John A.
Kekuda, Ramesh
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Rastelli, Luca
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Anderson, David W.
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Spytek, Kimberly A.
Edinger, Shlomit R.
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 ilarity 100.0%;
Conservative (
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71.8%; Score 1167; DB 15; 100.0%; Pred. No. 9.2e-113; tive 0; Mismatches 0;
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                                   Length
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Sequence 1914, Application US/09833245

Publication No. US20040010134A1

GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
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US-10-844-874-20
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US-09-833-245-1914
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; NAME/KEY: misc feature
; OTHER INFORMATION: rat alpha 2, 6-ST
US-10-844-874-20
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Publication No. US20040204381A1
GENERAL INFORMATION:
APPLICANT: Moskal, Joseph
APPLICANT: Yamamoto, Hirotaka
TITLE OF INVENTION: Detection and Treatment of Glyco-Enzyme-Related Disease
FILE REFERENCE: 97-186-E
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CURRENT FILING DATE: 2004-05-13
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
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TYPE: PRT
ORGANISM: Rat
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                                                                                                                                                                                                                                                                                                                                                                            QVYTETERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMVSDSYC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INVRTQEPL-QLNCNHCAVVSNSGQMVGQKVGEEIDRASCIWRMNNAPTKGFEEDVGYMT 123
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CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1915
LENGTH: 305
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PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199, 38
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1914
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US-09-833-245-1915
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US-09-833-245-1915
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Best Local
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                                                                                                                                             Matches
                                                                                                                                                                               Query Match
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TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546FCT
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TYPE: PRT
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                                                                                              HFSGYSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEAD 114
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                  VGQRSTLRVVSHTSVPLLLRNVSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTR 174
                                                                       HY-GYINVKTQEPLQLD-CDLCAIVSNSGQMVGQKVGNEIDRSSCIWRMNNAPTKGYEED
44.1%;
ilarity 52.7%;
Conservative 4
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52.7%; Pred. No. 1.2e-65;
ative 48; Mismatches 65
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                                                                                                                                               Score 716.5; DB 11,
Pred. No. 1.2e-65;
18; Mismatches 65;
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; LENGTH: 305
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-186-22
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US-10-188-186-22
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CURRENT FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: 60/303046
PRIOR FILLING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/360814
PRIOR FILLING DATE: 2002-03-01
PRIOR FILLING DATE: 2002-03-01
PRIOR FILLING DATE: 2001-09-07
PRIOR FILLING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 60/323380
PRIOR APPLICATION NUMBER: 60/323380
PRIOR APPLICATION NUMBER: 60/323380
PRIOR FILLING DATE: 2001-09-19
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Best Local S
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SEQ ID NO 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 368
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS
                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2002-04-19
APPLICATION NUMBER: 60/305673
FILING DATE: 2001-07-16
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APPLICATION NUMBER: 60/305262
FILING DATE: 2001-07-13
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FILING DATE: 2001-07-09
APPLICATION NUMBER: 60/304502
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                    239 NDTYCKTEGYRKVPYHYYEQGR-DECDEYFLHEHAPYGGHRFITEKKVFAKWAKKHRIIF
                                                                                                      179 IYPNAQIYUTTEKRMSYCDGVFKKETGKDRVQSGSYLSTGWFTFLLAMDACYGIHVYGMI
                                                                                                                                 175 MYPGLQVYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEBIVVYGMV
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                                               SDSYCREKSHPSVPYHYFEKGRLDECQMYLAHEQAPRSAHRFITEKAVFSRWAKKRPIVF
                                                                                                                                                                                           VGRMTMIRVVSHTSVPLLLKNPDYFFKEANTTIYVIWGPFRNMRKDGNGIVYNMLKKTVG
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US-10-188-186-24
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PRIOR FILING DATE:
NUMBER OF SEQ.ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2350
LENGTH: 305
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US-10-104-047-2350
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                                                         PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: 60/303828
PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 60/323380
PRIOR APPLICATION NUMBER: 60/323380
PRIOR APPLICATION NUMBER: 60/361133
PRIOR PILING DATE: 2002-03-01
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Best Local Similarity
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                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/303046
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/360814
                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/188,186
CURRENT FILING DATE: 2002-07-02
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CURRENT FILING DATE: 2002-03-25
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               APPLICATION NUMBER: 60/304016 FILING DATE: 2001-07-09
APPLICATION NUMBER: 60/304502
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PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 60/373881
PRIOR FILING DATE: 2002-04-19
PRIOR PELICATION NUMBER: 60/305673
PRIOR PELICATION NUMBER: 60/305673
PRIOR FILING DATE: 2001-07-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 368
SOFTWARE: Custom
SEQ ID NO 24
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/188,186
CURRENT FILING DATE: 2002-07-02
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING
Remaining Prior Application data removed - See File Wrapper or PALM.
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FILING DATE: 2002-03-01
APPLICATION NUMBER: 60/303828
                                  FILING DATE: 2001-07-16
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                                                                       FILING DATE: 2001-07-13
APPLICATION NUMBER: 60/373881
FILING DATE: 2002-04-19
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                                                       APPLICATION NUMBER: 60/305673
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Pred. No. 2.8e-63;
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                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR PILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR PILING DATE: 2001-03-14
PRIOR PILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR APPLICATION NUMBER: 60/324,967
                            PRIOR FILING DATE: 2001/09/26
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR FILING DATE: 2001-09-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 189, A Publication No.
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ORGANISM: Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VGRMTMIRVVSHTSVPLLLKNPDYFFKEANTTIYVIWGPFRNMRKDGNGIVYNMLKKTVG
FastSEQ
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Rachel E. MEYERS
Michael MORRISEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Manjula GANNAVARAPU
                                                                                                                                                                                                                                                                                                                                                                                   Xumei ZHAO
Karen GLATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gordon B. MILLS
Robert C. BAST, Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sebastian HOERSCH
Shubhangi KAMATKAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/10097340 o. US20030087250A1
                                                                                                                                                                                                                                                                                                                                                                                                                         Rosemarie SCHMANDT
                                                                                                                                                                                                                                                                                                                                                                                                                                         Karen LU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peter VEIBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peter OLANDT
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 for Windows Version
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PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2441
LENGTH: 336
TYPE: PRT
                                                                        ; ORGANISM: Homo sapiens
US-10-094-749-2441
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Query Match 39.3%;
Best Local Similarity 47.9%;
Matches 125; Conservative 4
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Best Local Similarity 47.9%;
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                                                                                                                                                                                                                                                                  APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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APPLICANT: SUGIY!
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blication No. US20030219741A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 MNDAPTRGYGRDVGNRTSLRVIAHSSIQRILRNRHDLLNVSQGTVFIFWGPSSYMRRDGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 MNQAPTVGFEADVGQRSTLRVVSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 TQQRPGVPAGPRPLDGYLGVADHKPL-KMHCRDCALVTSSGHLLHSRQGSQIDQTECVIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 TGSRPTVP-GPLHFSGYSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFR 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTSUKI, TEA.
OTSUKI, TEA.
WAKAMATSU, AI
SATO, HIROYUKI
SATO, SHIZUKO
TOULI, SHIZUKO
                                                                                                                                                                                                                                                                                                                                                                                            OTSUKA, KAORU
NAGAI, KEIICHI
IRIB, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
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SUGIYAMA, TU...
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 44; Mismatches
                  Score 639.5; DB 14;
Pred. No. 1.4e-57;
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   Indels
                                 Length 336;
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RESULT 15
US-10-288-252-11
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                                                                                                           PRIOR FILING DATE: 2000-
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PERL Program
SEQ ID NO 11
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Publication No. US20030143686A1
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: US 60/247,931
PRIOR FILING DATE: 2000-11-09
                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/252,819
PRIOR FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: US 60/249,639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: PI-0241 USA
                                                 LENGTH: 336
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                 FEATURE: NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030143686A1 2778782CD1
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                                                                                                                                                                                                           APPLICATION NUMBER: US 60/238,481 FILING DATE: 2000-10-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MNQAPTVGFEADVGQRSTLRVVSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VFSRWAKKRPIVFAHPSWRTE 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELCEEIVVYGMVSDSYCREKSHPSVPYHYFEKGRLDECQMYLAHEQAPR-SAHRFITEKA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GQVYNNLHLLSQVLPRLKAFMITRHKMLQFDELFKQETGKDRKISNTWLSTGWFTMTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELCDRINVYGMVPPDFCRDPNHPSVPYHYYEPFGPDECTMYLSHERGRKGSHHRFITEKR 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGSRPTVP-GPLHFSGYSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFR 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BURFORD, Neil
GANDHI, Ameena R.
WARREN, Bridget A.
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HAFALIA, April J.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YAO, Monique G.
TRIBOULEY, Cath
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                                                                                                                                                                   2000-09-29
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Search completed: December 21, 2004, 22:50:58 Job time : 79 secs
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                                                                                                          103 MNQAPTVGFEADVGQRSTLRVVSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLG 162
|| || || : || |::|| : :|| :: || :: || 1
123 MNDAPTRGYGRDVGNRTSLRVIAHSSIQRILRNRHDLLNVSQGTVFIFWGPSSYMRRDGK 182
                                                        303 VFKNWARTFNIHFFQPDWKPE 323
                                                                               282 VFSRWAKKRPIVFAHPSWRTE 302
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Result
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Maximum
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-MODEL=frame+_D2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10019114/runat_21122004_100141_3443/app_query.fasta_1.455
-Q=/cgn2_1/USPTO_spool/US10019114/runat_21122004_100141_3443/app_query.fasta_1.455
-DB=Issued_Patents_NA -QFMT=fastap_-SUPFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=set -HEARSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10019114 @CGN 1 1 69 @runat 21122004 100141 3443 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPDP=10 -XGAPDRT=0.5 -FGAPOP=6
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Maximum Match 100%
Listing first 45 summaries
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Fgapop 6.0,
Delop 6.0,
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-09-620-312D-401

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US-08-503-133A-1

US-08-576-775A-1

US-08-972-498-1

US-08-98-545-1

US-08-446-875-15

US-08-446-875-15

US-08-446-875-15

US-08-446-875-15

US-08-626-994A-4
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| 149             |            | 150.5            |          | 150.5    | 167       | 168          | 168             | 168          | 168          | 171      | 171              | 172          | 174.5     | 176              | 176       | 178          | 178      | 178         | 178      | 179           | 179      | 8.       |           | 8             | 8        | •               | ۳.              | 188.5      | 88.           | 90.         | •         | 90.             |
| 9.2             | •          | 9.3              | ٠        | 9.3 -    | •         | •            | 10.3            | •            | 10.3         | 10.5     | •                | •            | •         | •                | •         | 10.9         |          | •           | •        | •             | 11.0     | 11.6     |           | 11.6          |          | •               | •               | 11.6       | ٠             | 11.7        | •         | 11.7            |
| 2121            | 1766       | 76               | 15       | 1158     | 52        | 30           | 2304            | tπ           | 24           | 1146     | 1146             | 2117         | 1622      | 1206             | 1206      | 2671         | 2671     | 1206        | 1206     | 1188          | 1188     | 1682     | 1682      | 1682          | 1682     | 1292            | 1292            | 1292       | 1292          | 1660        | 1660      | 1048            |
| 4.              | _          | _                | N        | N        | 4         | ۳            | Ľ               | 4            | μ            | w        | N                | 4.           | w         | ຎ                | N         | ω            | N        | ω           | N        | N             | N        | ω        | N         | N             | Н        | ω               | N               | N          | _             | ω           | 1         | ω               |
| US-09-425-488-1 | -08-309-98 | US-07-991-587A-6 | 02-3850  | -08-4    | -140-002- | -08-446-777- | US-08-446-777-5 | -09-023-655- | -08-446-777- | -09-143- | US-08-666-367B-4 | -08-361-304A | -09-334-6 | US-08-102-385G-3 | -08-446-8 | -09-143-438- | -80-     | -09-143-438 |          | -08-102-385G- | 75       | -66      | -08-972-4 | -08-576-775A- | 90       | US-08-899-545-7 | US-08-972-498-7 | -08-576-77 | -08-503-133A- | -08-957-742 | -08-626-9 | US-08-957-742-4 |
|                 |            |                  |          |          |           |              |                 |              |              |          |                  |              |           |                  | `         |              |          |             |          |               |          |          |           |               |          |                 |                 |            |               |             |           |                 |
| Sequence        | Sequence   | Sequence         | Sequence | Sequence | Sequence  | Sequence     | Sequence        | Sequence     | Sequence     | Sequence | Sequence         | Sequence     | Sequence  | Sequence         | Sequence  | Sequence     | Sequence | Sequence    | Sequence | Sequence      | Sequence | Sequence | Sequence  | Sequence      | Sequence | Sequence        | Sequence        | Sequence   | Sequence      | Sequence    | Sequence  | Sequence        |
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| Appli           | Appli      | Appli            | Appl     | Appl     | l, App    | Appli        | Appli           | 50, Ap       | Appli        | Appli    | Appli            | Appli        | Appli     | Appli            | Appli     | Appli        | Appli    | Appli       | Appli    | Appli         | Appli    | Appli    | Appli     | Appli         | Appli    | Appli           | Appli           | Appli      | Appli         | Appli       | Appli     | Appli           |

## ALIGNMENTS

US-09-599-360B-25

```
Sequence 25, Application US/09599360B
Patent NO. 5548633
GENERAL INFORMATION:
APPLICANT: Domas Milne Edwards, J.B.
APPLICANT: Bougueleret, L.
APPLICANT: Jobert, S.
FILE REFERENCE: GENERI .050CP3
CURRENT APPLICATION: Complementary DNA's Encoding Proteins with Signal Peptides
FILE REPERENCE: GENERI .050CP3
CURRENT APPLICATION NUMBER: US/09/599,360B
CURRENT FILING DATE: 1990-16-21
PRIOR APPLICATION NUMBER: 60/113,686
PRIOR FILING DATE: 1999-16-25
PRIOR APPLICATION NUMBER: 60/141,032
PRIOR APPLICATION NUMBER: 60/141,032
PRIOR APPLICATION NUMBER: 60/141,032
PRIOR APPLICATION NUMBER: 60/141,032
PRIOR APPLICATION NUMBER: 09/469,099
PRIOR PILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patent.pm
SEQ ID NO 25
LENGTH: 1556
TYPE: DNA
CRAMISM: Homo Sapiens
FEATURE:
FEATURE:
FEATURE:
NAME/KEY: 615
COCATION: 261..1166
NAME/KEY: 615
COCATION: 261..314
COTHER INFORMATION: Score 8.80
COTHER INFORMATION: Seq RLVLLIILCSVVFS/AV
NAME/KEY: POLYA, Site
LOCATION: 1524..1556
USC-09-599-360B-25
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Best I Query DB:

: Local S. :y Match:

Percent Similarity:
Best Local Similarity:

3.61e-179 1626.00 100.00% 100.00% 100.00%

Length: Matches:

Pred. No.: Alignment

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US-10-019-114A-7 (1-302)

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AlaValPheSerArgTrpAlaLysLysArgProIleValPheAlaHisProSerTrpArg
                                                                                                               CAGATGTACCTGGCACGAGCAGGCGCCCCGAAGCGCCCACCGCTTCATCACTGAGAAG
                                                                                                                          GlnMetTyrLeuAlaHisGluGlnAlaProArgSerAlaHisArgPheIleThrGluLys
                                                                                                                                                                            GluLysSerHisProSerValProTyrHisTyrPheGluLysGlyArgLeuAspGluCys
                                                                                                                                                                                                                                           GCGCTGGAGCTGTGAGGAGATCGTGGTCTATGGGATGGTCAGCGACAGCTACTGCAGG
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Patent No. 6280989
GENERAL INFORMATION:
APPLICANT: Kapitonov, Dmitri
APPLICANT: Yu, Robert
TITILE OF INVENTION: NOVEL SIALYLTRANSFERASES
FILLE REFERENCE: VCUIP-6
CURRENT APPLICATION NUMBER: US/09/334,601
CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 94
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 2056
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Best Local Similarity:
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NAME/KEY: CDS
LOCATION: (181)..(1188)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo
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                                                                                                                                                                                                                                                                                                                                                                                         MetAsnGlnAlaProThrValGlyPheGluAlaAspValGlyGlnArgSerThrLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCGGACCACAAGCCCCTG---AAAATGCACTGCAGGGACTGTGCCCTGGTGACCAGCTCA
               GluLeuCysGluGluIleValValTyrGlyMetValSerAspSerTyrCysArgGluLys
                                                             ThrPheThrGluArgMetMetAlaTyrCysAspGlnIlePheGlnAspGluThrGlyLys
                                                                                                                                                                                                                                                                               AlaArgAspThrLeuTyrMetValTrpGlyGlnGlyArgHisMetAspArgValLeuGly :::::: | | | :::::: | | | | | | | |
                                                                                                                                                                                                                                                                                                                                             ValValSerHisThrSerValProLeuLeuLeuArgAsnTyrSerHisTyrPheGlnLys
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                                                                                                                                                                                                                            GlyArgThrTyrArgThrLeuLeuGlnLeuThrArgMetTyrProGlyLeuGlnValTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCCAGCAGCGCCCCGGGGTCCCCGGGGACCGGGCCACTGGACGGATACCTCGGAGTG
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 GAGCTCTGTGACAGGATCAATGTTTATGGCATGGTGCCCCCCAGACTTCTGCAGGGATCCC
                                                                                                                           ATGATTACTCGCCACAAGATGCTGCAGTTTGATGAGCTCTTCAAGCAGGAGACTGGCAAA
                                                                                                                                                                                               GGCCAGGTCTACAACAACCTGCATCTCCTGAGCCAGGTGCTGCCCCGGCTGAAGGCCTTC
                                                                                                                                                                                                                                                              AGCCAGGGCACCGTGTTCATCTTCTGGGGCCCCAGCAGCTACATGCGGCGGGACGGCAAG
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Matches:
Conservative:
Mismatches:
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APPLICANT: Mang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: Unn Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILB REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER: PRIOR FILING DATE: 2000-01-21
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Best Local Similarity:
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                                                                                                                                                                                    Query Match:
                                                                                                                                                                                                                                                                            Alignment Scores:
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SOFTWARE: pt FL genes Version 1.0
SEQ ID NO 401
LENGTH: 2697
TYPE: DNA
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                323 TGCCAATGAGGTCTTCCATTACGGCTC---
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        46 SerArgProThrValProGlyProLeu--
                                                                      CysTrpAlaGlyLeuProLeuCysLeuAlaThrCysLeuAspHisHisPheProThrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCTTTAAGAACTGGGCACGGACATTCAATATTCACTTTTTTCAACCAGACTGGAAACCA 1146
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Asundi, Vinod
Zhang, Jie
Ren, Feiyan
Chen, Rui-hong
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Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
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Matches:
        ----HisPhe-SerGlyTyrSerSerVa
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                                                                          GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
ITITLE OF INVENTION: ESTS and Encoded Human FILTE OF INVENTION: ESTS and Encoded Human FILE REFERENCE: GENSET 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOPTWARE: Patent.pm
SEQ ID NO 55
LENGTH: 546
TYPE: DNA
ORGANISM: Homo mapiens
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US-09-621-976-55
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                                                                                                                                                                                                                                                                                                                                                    Sequence 55, Application US/09621976 Patent No. 6639063
FEATURE:
NAME/KEY: CDS
LOCATION: 260..544
NAME/KEY: sig_peptide
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Best Local Similari
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OTHER INFO
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                                                                                                                                                                                                                                                                                                                       APPLICANT: Gerardy-Schahn, Rita; Fukuda, Minoru;
APPLICANT: Nakayama, Jun; Eckhardt, Matthias
TITLE OF INVENTION: Isolated Polysialyl Transferases,
TITLE OF INVENTION: Nucleic Acid Molecules Coding Therefor,
TITLE OF INVENTION: Production and Use
                                                                                                   SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
CURRENT APPLICATION UNMBER: US/08/503,133A
FILING DATE: 17-JULY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Disketto
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC
     NAME: Hanson, No. 5747326man D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                               APPLICATION NUMBER: PCT/EP94/04289
FILING DATE: 22-DEC-1994
ATTORNEY/AGENT INFORMATION:
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US-10-019-114A-7 (1-302) x US-08-503-133A-1 (1-2026)
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Best Local Similarity:
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US-08-576-775A-1
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Patent No. 5849904
GENERAL INFORMATION:
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FILING DATE: 21-December-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/503,133
FILING DATE: 17-July-1995
PRIOR APPLICATION DATA:
APPLICATION UMBER: PCT/EP94/04289
FILING DATE: 22-December-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212) 838-3884 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 111
MOLECULE TYPE:
FEATURE:
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TITLE OF INVENTION: Nucleic Acid Molecules Coding Therefor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BO
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Diskett
COMPUTER: IBM PS/2
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LOCATION:
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SOFTWARE: Wordper
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Gerardy-Schahn, Rita; Fukuda, Minoru;
APPLICANT: Nakayama, Jun; Eckhardt, Matthias
TITLE OF INVENTION: Isolated Polysialyl Transferases,
TITLE OF INVENTION: Nucleic Acid Molecules Coding Therefor, Methods of
TITLE OF INVENTION: Production and Use
                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 21-Dece
                                                                                                                                                                    COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DO
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 8
                                                                                             FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                       CITY: New York City
STATE: New York
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APPLICATION NUMBER:
                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                           COUNTRY: U
ZIP: 10022
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                                                                                                                                                                                                                                                                                                                                                                                                                        805 Third Avenue
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IBM PS/2
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                    21-December-1995
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Best Local Similarity:
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INFORMATION FOR SEQ ID NO: 1:
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NAME: Hanson, No. 5959078man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
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PRIOR APPLICATION DATA:
APPLICATION UNMER: PCT/EP94/04289
FILING DATE: 22-December-1994
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LOCATION:
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nucleic acid
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                uCysGluGluIleValValTyrGlyMetValSerAspSerTyrCysArgGluLysSerHi 244
                                                                                                                                         TGTCAGAGGTTACTGGCT----
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                                                                                                      gArgGlnSerGlySerPheLeuSerThrGlyTrpPheThrMetIleLeuAlaLeuGluLe
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TTGTGATGAAATTCACCTGTATGGGTTCTGG-----CCCTTCCCTAAGGATTTGAATGG 1226
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12.08%
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Matches:
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59 TyrSerSerValProAspGlyLysProLeuValArgGluProCysArgSerCysAlaVal 78 ::::||| ::::|||::::|||||||||||

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                                            Percent Similarity:
Best Local Similarity:
Query Match:
US-10-019-114A-7 (1-302) x US-08-899-545-1 (1-2026)
                                                                                                              Pred. No.:
                                                                                                                           Alignment Scores:
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; LOCATION:
US-08-899-545-1
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APPLICANT: Gerard
                                                                                                                                                                                                                                                                                                                 TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: HANSON, NO. 6020201ma
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BO
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 2026 base pair
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MEDIUM TYPE: Diskett
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                TYPE: nucleic acid
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T: 805 Third Avenue
New York City
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NVENTION: Isolated Polysialyl Transferases,
NVENTION: Nucleic Acid Molecules Coding Therefor, Methods
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                                               1.47e-12
196.50
45.93%
28.86%
12.08%
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                                                  Conservative: Mismatches: Indels:
                                  Gaps:
                                                                                               Length:
Matches:
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US-08-446-875-15
Sequence 15, Application US/08446875
Patent No. 5858751
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                     APPLICANT: I
APPLICANT: I
APPLICANT: I
APPLICANT: O
APPLICANT: I
                                                                                                                                                                 APPLICANT: Burlingame, Alma L.

APPLICANT: Medzihradszky, Katalin

TITLE OF INVENTION: Compositions and Methods for the

NUMBER OF SEQUENCES: 16

CONDUCTOR: 16
                                                                                                                                                   CORRESPONDENCE ADDRESS:
  COMPUTER READABLE FORM:
                                                                                STREET: 2029 Centu
CITY: Los Angeles
                                           COUNTRY:
                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 rargTrpalaLysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 sProSerValProTyrHisTyrPheGluLysGlyArgLeuAspGluCysGlnMetTyrLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 ThrTyrArgThrLeuLeuGlnLeuThrArgMetTyrProGlyLeuGlnValTyrThrPhe 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 Tyr$er-------HisTyrPheGlnLysAlaArgAspThrLeu-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         793 TTTGTAATCAGGTGCAATCTAGCTCCTGTGGTGGAGTTTGCTGCGGATGTGGGGGACTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              733 GTTGGAAACTCTGGCATTCTACTAGACAGTGGATGTGGCAAGGAGATTGACAGTCACAAT 792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 CysValPheArgMetAsnGlnAlaProThrValGlyPheGluAlaAspValGlyGlnArg
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                         90067
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                                                                     S
                                                                                                        2029 Century Park East,
                                                                                                                                                                                                                                                                                                          Wen, Xiaohong
Livingston, Brian Duane
Gillespie, William
                                           USA
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                                                                                                                                   Poms, Smith, Lande & Rose
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                                                                                                            Suite 3800
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Ouery Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-019-114A-7 (1-302) x US-08-446-875-15 (1-1020)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-446-875-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/102,385
APPLICATION NUMBER: 08/102,385
FILING DATE: August 4, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE,DOCKET NUMBER: 111-197
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1788-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (310) 277-12: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING-SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US FILING DATE: July 12,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                              171
  832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           475 GAGATAGACAGTCACGACTTTGTCCTCAGGATGAACAAGGCGCCCACGGCAGGGTTTGAA
                                                                                                                                                                                                                                                                  700 CCTGCAAAGATCAGAGTGAAACAGGATAAGATCCTGATCTACCACCCAGCCTTCATCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     415 TGCCGGCGCTGCGCCGTTGTGGGCCAACTCGGGCAACCTGAGGGAGTCTTCTTATGGGCCT 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 GluIleAspSerAlaGluCysValPheArgMetAsnGlnAlaProThrValGlyPheGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 CysArgSerCysAlaValValSerSerSerGlyGlnMetLeuGlySerGlyLeuGlyAla
  ATGCATGTCTGCGATGAGGTGGACTTGTACGGCTTCGGGGCAGACAGC-----AAAGGG
                              LeuGluLeuCysGluGluIleValValTyrGlyMetValSerAspSerTyrCysArgGlu 241
                                                                                                                                                                                                                                                                                                                                                                                                    GlnGlyArgHisMetAspArgValLeuGlyGlyArgThrTyrArgThrLeuLeu-----
                                                                                                                               LysAsnArgArgGlnSerGlySerPheLeuSerThrGlyTrpPheThrMetIleLeuAla
                                                                                                                                                                           TATGTCTTTGACAACTGGCTGCAAGGGCAC--
                                                                                                                                                                                                                       TyrThrPheThrGluArgMetMetAlaTyrCysAspGlnIlePheGlnAspGluThrGly 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                CCACATAATGTCAGCATGATCCTGGTGCCCTTCAAG---ACCATCGACTTGGAGTGG---
                                                                                                                                                                                                                                                                                                                                                          -----GTGGTGAGCGCCATCACCACGGCACCATTTCCCACACCTACATCCCGGTT
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Matches:
Conservative:
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US-10-019-114A-7 (1-302) x US-08-446-875-1 (1-1218)
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION LDATA:
APPLICATION NUMBER: US/08/446,875
FILING DATE: July 12, 1995
CLASSIFICATION NUMBER: 08/102,385
PRIOR APPLICATION NUMBER: 08/102,385
FILING DATE: August 4, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 111-197
TELECOMPUNICATION: NIFORMATION:
TELEPAX: (310) 788-5000
TELEPAX: (310) 778-5000
TELEPAX: (310) 778-5000
TELEPAX: (310) 778-5000
TELEPAX: (310) 277-1297
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECTILE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-08-446-875-1
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                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                Alignment Scores: Pred. No.:
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Patent No. 5858751
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NAME/KEY: CDS
LOCATION: 91..1119
OTHER INFORMATION: /
OTHER INFORMATION: C
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APPLICANT:
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APPLICANT: Kelm, Sorge
APPLICANT: Burlingame, Alma L.
APPLICANT: Medzihradszky, Katalin
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Identification and Synthesis of Sialyltransferases
                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Poms, Smi
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CITY: Los Angeles
STATE: CA
                                                                                                                                                                                                                                                                                                                          ORGANISM: porcine TISSUE TYPE: liver, submaxillary glands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 90067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 LysSerHisProSerValProTyrHisTyrPheGlu
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2029 Century Park East, Suite 3800
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Wen, Xiaohong
Livingston, Brian Duane
Gillespie, William
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192.50
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GalNAc alpha 2,3 sialyltransferase"
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Matches:
Conservative:
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Indels:
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|---|--------------|--|---|--|-----|--|--------------------------------------|-------|-----|-----------------------------------|---|---|---|-----|--|--|---|-----|---|------------------------------------|---|
| Sequence 1, Application US/0810238 Sequence 1, Application US/0810238 Patent No. 5962294 GENERAL INFORMATION: APPLICANT: Faulson, James C. APPLICANT: Wen, Xiaohong APPLICANT: Gillespie, William APPLICANT: Kelm, Sorge APPLICANT: Medzihradszky, Kata TITLE OF INVENTION: Identifica TITLE OF INVENTION: Identifica NUMBER OF SEQUENCES: 36 CORRESPONDENCE ADDRESS: ADDRESSEE: Oppenheimer Wolff STREET: 2029 Century Park Ea COUNTRY: USA COUNTRY: USA COUNTRY: USA ZIP: 90067 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: Floppy disk COMPUTER: Floppy disk COMPUTER: Floppy disk COMPUTER: Patentin Release # CURRENT APPLICATION DATA: | 211 m 11 y/0 | 236  | 915   | 216  | 855 | 196 eGlnAspGlu                             | 176 rProGlyLeu<br>   <br>798 CCCCGCC | 738   | 156 | Db 705 CAGC                       | 136 rSerHis   | 645   | 116 y   | 585 | 96   | 525  | 76  | 484 | 59 rSerSerValProAspGly                      | 444                                | 40  |
| Duane alin ons and Methods for the ation and Synthesis of Sialyltransferases att. 38th Floor BDOS BDOS BDOS BDOS BDOS BDOS BDOS BDOS  | Chaine       | erTyrCysArgGluLysSerHisProSerValProTyrHisTyrPheGlu 253 | CTCCGTGATCTTCTCCCTGCACATCTGTGACGACGAGGTGGACTTGTATGGCTTTGGGGCGGA 97. | LeuCysGluGluIleValValTyrGlyMetValSerAs 236 | 9   | ArqArqGlnSerGlySerPheLeuSerThrGlyTrpPh 216 | 1961\frac{1}{2}                      | GT 79 |     | ATGATCCTGGTCCCCTTCAAGACCACCGA 737 | TyrPheGlnLysAlaArgAspThrLeuTyrMetValTrpGlyGlnGlyArgHi 156 | :::::   <br>  GAGCAAGACCACCCACCATTTCGTGTACCCCGAGAGCTTCCGGGAAGCTGGCGCAGGAGGT 704 | GlnArgSerThrLeuArgValValSerHisThrSerValProLeuLeuLeuArgAsnTy 136 | ::: | AsnGlnAlaProThrValGlyPheGluAlaAspValGl 116 | AACCTGAAGGAGTCCTACTATGGGCCTCAGATAGACAG 584 | sAlaValValSerSerSerGlyGlnMetLeuGlySerGlyLeuGlyAlaGluIleAspSe 96 | н.  | roAspGlyLysProLeuValArgGluProCysArgSerCy 76 | CAGGGAGCTGTTCCAGGTGGTGCCTGGGAACGTG | HisHisPheProThrGlySerArgPro-ThrValProGlyProLeuHisPheSerGlyTy 59 |

APPLICATION NUMBER:

04-AUG-1993

US/08/102,385G

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/925369 FILING DATE: 04-AUG-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 04-AUG-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 97
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LOCATION:
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
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                                    176 rProGlyLeuGlnValTyrThrPheThrGluArgMetMetAlaTyrCysAspGlnIlePh 196
                                                                                                                                                                                                                                                                        116 yGlnArgSerThrLeuArgValValSerHisThrSerValProLeuLeuLeuArgAsnTy 136
  798
                                                                                                                156 sMetAspArgValLeuGlyGlyArgThrTyrArgThrLeuLeuGlnLeuThrArgMetTy
                                                                                                                                                                                            136 rSerHisTyrPheGlnLysAlaArgAspThrLeuTyrMetValTrpGlyGlnGlyArgHi 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      444 CACCAT-----CAGGGAGCTGTTCCAGGTGGTGCCTGGGAACGTG-----
                                                                                                                                                                                                                                                                                                                                       96 rAlaGluCysValPheArgMetAsnGlnAlaProThrValGlyPheGluAlaAspValGl 116
                                                                                                                                                                                                                                                                                                                                                                                                                                 76 sAlaValValSerSerSerGlyGlnMetLeuGlySerGlyLeuGlyAlaGluIleAspSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 rSerSerValProAspGlyLysProLeuValArgGlu-----ProCysArgSerCy
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CCCCGCC---AAGATCAAAGTCAAAAAGGAGAAGATCCTGATTTATCACCCGGCCTTCAT 854
                                                                             CCTGGAGTGGGTGATCAGCGCCACCACCGGCACCATCTCCCCACACCTACGTTCCTGT
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GalNAc alpha 2,3 sialyltransferase"
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Matches:
Conservative:
Mismatches:
Indels:
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US-08-626-994A-4
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APPLICANT: Shuich
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MEDIUM TYPE: 1.44 diskette
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1+ (ASCII)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7'
FILING DATE: April 3, 19;
ATTORNEY/AGENT INFORMATION:
NAME: Arnold Turk
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Sia'.2,3Gala 1,4GlcNAc'
TITLE OF INVENTION: SIALYLTRANSFERASE
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386 GGAAACAĞTGĞAATCTTGACAGĞĞAĞTCAGTĞTĞĞACAAĞAAATAĞATAAATCAĞATTTT 445
                                                                    326 TCCCTGCTCCCAGATGTGTCGCCCATTATGAATAAGCGTTATAATGTTTGTGCTGTGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 eGlnAspGluThrGlyLysAsnArgArgGlnSerGlySerPheLeuSerThrGlyTrpPh 216
                            80 SerSerSerGlyGlnMetLeuGlySerGlyLeuGlyAlaGluIleAspSerAlaGluCys 99
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30.95%
11.72%
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Matches:
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RESULT 13
US-08-957-742-4
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Patent No. 6017743
GENERAL INFORMATION:
                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/626,994
FILING DATE: April 3, 1996
APPLICATION NUMBER: JP 77469/1995
FILING DATE: April 3, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold Turk
                                                                                                                                                                                                                                                                        MEDIUM TYPE: 1.44 diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1+ (ASCII)
CURRENT APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION: Sia' 2,3Gala 1,4G1CNAC'
TITLE OF INVENTION: SIALYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                       ZIP: 20191
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 di
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CORRESPONDENCE ADDRESS:
             REGISTRATION NUMBER: 33,094
REFERENCE/DOCKET NUMBER: P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 716-1191
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                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATACTTTGGATCCCTGCATTTTTCTTCCACACTTCTGCAACTGTAACGAGAACGCTAGTG
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(703) 71
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   716-1180
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LENGTH: 1048 bases
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
US-08-957-742-4
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                                                                                                GENERAL INFORMATION:
APPLICANT: Shuich
                   APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION: Sia' 2,3Gala 1,4G1CNAC
TITLE OF INVENTION: SIALYLTRANSFERASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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       ADDRESSEE:
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       Greenblum & Bernstein,
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Best Local Similarity:
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APPLICATION NUMBER: JP 774.
FILING DATE: April 3, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold Turk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 716-1191 TELEFAX: (703) 716-1180
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OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1+ (ASCII)
CURRENT APPLICATION DATA:
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STRANDEDNESS: not relevant
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REFERENCE/DOCKET NUMBER: P1
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                                          190 AlaTyrCysAspGlnIlePheGln-----AspGluThrGlyLysAspArgArgGlnSer
                                                                                      858 GATTTTTTTGTTGAGCACAGAGGTCAGTTAAAGGTC------CAGTTG 899
                                                                                                                            171 GlnLeuThrArgMetTyrProGly---LeuGlnValTyrThrPheThrGluArgMetMet 189
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Indels:
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Percent Similarity:
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Query Match:
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US-08-957-742-2
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Patent No. 6017743
GENERAL INFORMATION:
APPLICANT: Shuichi TSUJI et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/626,994
FILING DATE: April 3, 1996
APPLICATION NUMBER: JP 77469/1995
FILING DATE: April 3, 1995
FILING DATE: April 3, 1995
ATTORNEY/AGENT INFORMATION:
NAME: ATTOID TURK
REGISTRATION NUMBER: 33,094
REFERENCE/DOCKET NUMBER: P14595
TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 di
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LENGTH: 1660 bases
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PRIOR APPLICATION DATA:
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TITLE OF INVENTION: Sia' 2,3Gala 1,4G1CNAC '
TITLE OF INVENTION: SIALYLTRANSFERASE
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                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: not relevant
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                                       208 GlySerPheLeuSerThrGlyTrpPheThrMetIleLeuAlaLeuGluLeuCysGluGlu
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80 SerSerSerGlyGlnMetLeuGlySerGlyLeuGlyAlaGluIleAspSerAlaGluCys 99
                                                                          60 SerSerValProAspGlyLysProLeuValArgGluProCysArgSerCysAlaValVal
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1941 Roland Clarke Place
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Matches:
Conservative:
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Search completed: December 21, 2004, 22:52:56
Job time : 113 secs
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                                                                  245 ProSerValProTyrHisTyrPheGluLys 254
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1071 ---GATCTGCCCTACCACTACTATGACAAA 1097
                                                                                                                                 171 GlnLeuThrArgMetTyrProGly---LeuGlnValTyrThrPheThrGluArgMetMet 189
::: || | | | ::: || |
858 GATTTTTTGTTGAGCACAGAGGTCAGTTAAAGGTC------CAGTTG 899
                                                                                                                                                                                                                                                                                                                                                                                                       798 ATACTTTGGATCCCTGCATTTTTCTTCCACACTTCTGCAACTGTAACGAGAACGCTAGTG 857
                                                                                                                                                                                                                                                                                                                                                                                                                            160 ValLeu-----GlyGlyArgThrTyrArgThrLeuLeu 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      738 CTTTTAACCATTCAGGACCGTAACAACTTCTTCCTCAGTTTAAAAAAGCTTGATGGGGCC 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 PheGlnLysAlaArgAspThrLeuTyrMetValTrpGlyGlnGlyArgHisMetAspArg 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         690 AACCTCACA-----ACCTTCAATCCGAGCATCTTAGAGAAATATTACAACAAT 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 ThrLeuArgValValSerHisThrSerValProLeuLeuLeuArgAsnTyrSerHisTyr 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         570 GGAAACAGTGGAATCTTGACAGGGAGTCAGTGTGGACAAGAATAGATAATCAGATTTT 629
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Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlh
-MODEL-frame+ p2n.model -DEV=xlh
-Q-/cgm2 1/USFTO spool/US10019114/runat 21122004 100142 3479/app query.fasta_1.455
-Q-/cgm2 1/USFTO spool/US10019114/runat 21122004 100142 3479/app query.fasta_1.455
-DB=Published Applications NA -QFMT=fastap -SUFFTX=rnpb -MINMATCH=0.1
-LOOPCL-0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptto -NORM=ext -HEAPSITE=500 -MINLEN=0
-MAXIEN=2000000000 -USER=US10019114 @CGR 1 1 480 @runat 21122004 100142 3479
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
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Ygapop 10.0 , y
Fgapop 6.0 , E
Delop 6.0 , I
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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/ Cgn2_6/ptodata/1/pubpna/US09_BUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US09_BUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US09_NEW_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                         _6/ptodata/1/pubpna/US08 NEW PUB.seq:*
_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 44                | ı.         | , i   | ۱۵.            | 42             | 41             | 40                | 39           | 38             | ) (       | J (            | 36             | 35   | 34           |              | 2 6          | ا د          | 31           | 30           | 29                | 28           |              |              |              |              | 23           | 22         | 12           | 20           | 14         | 1 1          | 1.7           | 16             | 15           | 14              | 13             | 12           | 11        |              | 9             | 8          | 7             | 6               | , UT           | 4.            |                 | , V.            | , _           | Result      |
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| 44.               |            | 1 1   | 4              | 44             | 44.            | 44.               |              | 44             | : :       | 4              | 44             | 44.  |              | 4            |              |              | 44           | 44.          | 544.5             | 4.           | 44.          | 44.          | 44.          | 44           | 44.          | 44.        | 44           | 4.           | 44.        | 4.           | 6             | 36.            | 36.          | 9               | 39.            | 684          | 700.5     | 720          | 721           | 721        | 738           | 812             | 198            | 1605          | 1622            | N               | 1626          | Score       |
| •                 |            |   | ٠,             | ω.             | 33.5           | 'n                | 33.5         |                | ٠         | ٠,             | u              | 33.5 |              | ٠            | ٠,           |              | u            | u            |                   | ·            | ٠            | 33.5         | ·            | ω.           | 33.5         | ٠.         |              |              |            | 1 (J         | ۳.            | 9              | 9.           | 39.3            |                | 42.1         | 43.1      | 44.3         | 44.3          | 44.3       | ٠             | .9              | ·Ψ             | œ             | ٠               | ۰.              | 8             | Query       |
| 2401              | 1017       | 101   | 3401           | 2401           | 2401           | 2401              | 2401         | 2401           | 1017      | 3401           | 2401           | 2401 | 2401         | T017         | 101          | 3401         | 2401         | 2401         | 2401              | 2401         | 2401         | 2401         | 2401         | 2401         | 2401         | 2401       | 2401         | 2401         | 2401       | 2401         | 7.102         | 2075           | 2075         | 2090            | 2048           | 1106         | 1005      | 3207         | 3283          | 966        | 2956          | · w             | . 4            | 1151          | 1/35            | י ט             | 1556          | Length      |
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| US-10-176-492-205 | 01-0/1-0T- | 7 - L - L - L - C - C | -10-175-743-20 | -10-175-740-20 | -10-175-739-20 | US-10-174-588-205 | -10-174-582- | -10-174-579-20 | 70-11-01- | -10-174-673-30 | -10-173-700-20 |      | -10-180-552- | -TU-T/6-913- | -10-176-757- | -10-176-757- | -10-176-482- | -10-175-752- | US-10-175-738-205 | -10-173-706- | -10-176-915- | -10-176-914- | -10-176-749- | -10-176-483- | -10-174-581- | -10-175-73 | -10-176-758- | -10-174-590- | -10-052-58 | -09-946-374- | -10-108-260A- | -10-398-038-31 | S-10-288-252 | S-10-094-749-80 | S-10-097-340-1 | -10-188-186- | -10-188-1 | -10-104-047- | -10-198-846-1 | 0-188-186- | S-10-844-874- | S-09-895-298-   | 09-823-245A-30 | S-10-262-511- | S-09-895-298-15 | S-10-315-664-   | S-09-978-360A | ID          |
| equence 205,      | eduetice 7 | 2 10 10 10 10 10 10 10 10 10 10 10 10 10  | equence ons    | equence 205.   | 205,           | 205,              | 205,         | 205,           | ,         | 0 0            | 205            | 205, | 205,         | 205,         | 200          | 0 (          | 205          | 205,         | 205,              | 205,         | 205,         | 205,         | 205,         | 205,         | 205,         | 205,       | 205,         | 205,         | 205,       |              | 895,          | 31,            | 31,          | 802,            | 188,           | 19,          | 23, App   | w            | 1153          | 21,        | 19, App       | equence 121, Ap | quence 30, A   | Sequence 183, | equence 15, /   | equence 25, App | equence 2, A  | Description |

## ALIGNMENTS

| ٠.                                      | ٠.                            | ٠.                                      | ٠.                            | ٠.                                      | ٠.                            | ٠.                                      | ٠.                              | ٠.   | ٠.                         | ٠.   | ٠.                | ٠.              | ٠.                 | ٠.               | ٠.  | ٠.                   | ••                              | ٠.                                   | S                | RE       |
|---|-------------------------------|---|-------------------------------|---|-------------------------------|---|---------------------------------|--|----------------------------|--|-------------------|-----------------|--------------------|------------------|---|----------------------|---------------------------------|--------------------------------------|------------------|----------|
| PRIOR APPLICAT                          | PRIOR FILING D                | PRIOR APPLICAT                          | PRIOR FILING D                | PRIOR APPLICAT                          | PRIOR FILING D                | PRIOR APPLICAT                          | CURRENT FILING                  | CURRENT APPLIC                             | FILE REFERENCE: 56.US4.CIP | TITLE OF INVEN   | APPLICANT: Cl     | APPLICANT: Jo   | APPLICANT: Bo      | APPLICANT: Du    | APPLICANT: Edw                                | GENERAL INFORMATION: | Publication No. US20040110939A1 | Sequence 2, Application US/09978360A | US-09-978-360A-2 | RESULT 1 |
| PRIOR APPLICATION NUMBER: US 60/081,563 | PRIOR FILING DATE: 1998-02-09 | PRIOR APPLICATION NUMBER: US 60/074,121 | PRIOR FILING DATE: 1997-12-17 | PRIOR APPLICATION NUMBER: US 60/069,957 | PRIOR FILING DATE: 1997-11-13 | PRIOR APPLICATION NUMBER: US 60/066,677 | CURRENT FILING DATE: 2001-10-15 | CURRENT APPLICATION NUMBER: US/09/978,360A | : 56.US4.CIP               | TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides | Clusel, Catherine | Jobert, Severin | Bougueleret, Lydie | Duclert, Aymeric | APPLICANT: Edwards, Jean-Baptiste Dumas Milne | TION:                | US20040110939A                  | lication US/099                      |                  |          |
| 60/081,563                              |                               | 60/074,121                              | •                             | 60/069,957                              |                               | 60/066,677                              | )-15                            | JS/09/978,360A                             |                            | ntary DNA's En   |                   |                 | e                  |                  | iste Dumas Mi                                 |                      | =                               | 78360A                               |                  |          |
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Percent Similarity:
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PRIOR APPLICATION NUMBER: US 60/096,116
PRIOR APPLICATION NUMBER: US 60/099,273
PRIOR APPLICATION NUMBER: US 60/099,273
PRIOR PILING DATE: -09-04
PRIOR PILING DATE: -09-04
PRIOR PILING DATE: 1998-11-13
PRIOR PILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: US 09/215,435
PRIOR FILING DATE: 1998-12-17
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: CT//IB98/02122
PRIOR APPLICATION NUMBER: US 09/247,155
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: US 09/247,155
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 261..1166
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LENGTH: 1556
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NAME/KEY: sig_peptide
LOCATION: 261..314
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 8.80
OTHER INFORMATION: seq RLVLIILCSVVFS/AV
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GlnLysAlaArgAspThrLeuTyrMetValTrpGlyGlnGlyArgHisMetAspArgVal 160
                                                                 LeuArgValValSerHisThrSerValProLeuLeuLeuArgAsnTyrSerHisTyrPhe 140
                                                                                                                                           PheArgMetAsnGlnAlaProThrValGlvPheGluAlaAspValGlyGlnArgSerThr
                                                                                                                                                                                                                SerSerGlyGlnMetLeuGlySerGlyLeuGlyAlaGluIleAspSerAlaGluCysVal
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                                            CTGCGTGTCGTCACACACAGCGTGCCGCTGCTGCTGCGCAACTATTCACACTACTTC
                                                                                                                    TTCCGCATGAACCAGGCGCCACCGTGGGCTTTGAGGCGGATGTGGGCCAGCGCAGCACC
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Jobert, S.
APPLICANT: Jobert, S.
TITLE OF INVENTION: Complementary DNA's Encoding Pro
TITLE OF INVENTION: Peptides
FILE REFERENCE: GENSET.050CP3
CURRENT APPLICATION NUMBER: US/10/315,664
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US/99/599,360
PRIOR APPLICATION NUMBER: 60/113,686
PRIOR FILING DATE: 1900-06-21
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/141,032
PRIOR APPLICATION NUMBER: 60/141,032
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/469,099
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patent.pm
SEQ ID NO 25
LENGTH: 1556
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US-10-315-664-25
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                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
                               FEATURE:
NAME/KZ: sig_peptide
LOCATION: 261..314
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 8.80
OTHER INFORMATION: seq RLVLIILCSVVFS/AV
                                                                                                                                            NAME/KEY: CDS
LOCATION: 261..1166
NAME/KEY: polyA_site
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; LOCATION: 1524..1556 US-10-315-664-25

Percent Similarity:
Best Local Similarity:
Query Match:
DB:

1.17e-196 1626.00 100.00% 100.00% 100.00% 15

No:

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US-10-019-114A-7 (1-302) x US-10-315-664-25 (1-1556)
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                                    AlaValPheSerArgTrpAlaLysLysArgProIleValPheAlaHisProSerTrpArg
                                                                                                          GlnMetTyrLeuAlaHisGluGlnAlaProArgSerAlaHisArgPheIleThrGluLys
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                    GCGGTCTTCTCCCGCTGGGCCAAGAAGAGGCCCATCGTGTTCGCCCATCCGTCCTGGAGG
                                                                                        CAGATGTACCTGGCACACGAGCAGGCGCCCCGAAGCGCCCACCGCTTCATCACTGAGAAG
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CURRENT APPLICATION NUMBER: US/09/895,298

CURRENT FILING DATE: 2001-07-02

PRIOR APPLICATION NUMBER: 09/591,16

PRIOR APPLICATION NUMBER: 09/591,16

PRIOR APPLICATION NUMBER: PCT/US99/29950

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: 60/113,006

PRIOR APPLICATION NUMBER: 60/113,006

PRIOR APPLICATION NUMBER: 60/112,809

PRIOR APPLICATION NUMBER: 60/112,809

PRIOR FILING DATE: 1998-12-17

NUMBER OF SEQ ID NOS: 231

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 15

LENGTH: 1735
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; NAME/KEY: SITE
; LOCATION: (1002)
; OTHER INFORMATION: n
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Best Local Similarity:
Query Match:
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US-09-895-298-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application US/09895298
Publication No. US20030078405A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 47 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
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GlnLysAlaArgAspThrLeuTyrMetValTrpGlyGlnGlyArgHisMetAspArgVal 160
                                                                                                                                                                                                                                                                                                                                       HisPheProThrGlySerArgProThrValProGlyProLeuHisPheSerGlyTyrSer
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                                               LeuArgValValSerHisThrSerValProLeuLeuLeuArgAsnTyrSerHisTyrPhe 140
                                                                                                                                                                                           SerSerGlyGlnMetLeuGlySerGlyLeuGlyAlaGluIleAspSerAlaGluCysVal 100
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                                                                                                                       PheArgMetAsnGlnAlaProThrValGlyPheGluAlaAspValGlyGlnArgSerThr 120
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RESULT 4
US-10-262-511-183
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APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Kekuda, Ramesh
APPLICANT: Li, Li
APPLICANT: Li, Li
APPLICANT: Guo, Xiaojia (Sash
APPLICANT: Patturajan, Meera
APPLICANT: Spytek, Kimbarly A
APPLICANT: Edinger, Shlomit R
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 183, A Publication No.
APPLICANT: Shimkets, Richard A.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
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Miller Charles E.
Rastelli, Luca
Stone, David J.
Pena, Carol E. A.
Shenoy, Suresh G.
Shimkets, Richard A.
Rothenberg, Mark E.
Leach, Martin D.
Agee, Michele L.
Rothele L.
Rothers E.
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Malyankar, Uriel M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
                                                                                                                                                                                                                                                                                               Catterton, Elina
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Anderson, David W.
                                                                                                                                                                                                                                                                                                                                                                      Gorman, Linda
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o. US20040038223A1
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; OTHER INFORMATION: Wherein n
US-10-262-511-183
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PRIOR FILLING DATE: 2002-05-16
PRIOR PELLONGTION NUMBER: 60/328,056
PRIOR FILLING DATE: 2001-10-09
PRIOR PELLONGTION NUMBER: 60/373,260
PRIOR APPLICATION NUMBER: 60/373,826
PRIOR PILLING DATE: 2002-04-17
PRIOR PELLONGTION NUMBER: 60/373,826
PRIOR PILLING DATE: 2002-04-19
PRIOR PILLING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,435
PRIOR PILLING DATE: 2001-10-05
PRIOR PILLING DATE: 2001-10-05
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PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR FILING DATE: 2002-05-17
PRIOR FILING DATE: 2002-05-17
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NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 183
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (421)..(1074)
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NAME/KEY: misc_feature
LOCATION: (2)..(2)
OTHER INFORMATION: Wherein n may be
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                                        GlnAlaProThrValGlyPheGluAlaAspValGlyGlnArgSerThrLeuArgValVal
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Publication No. US20020039760A1
GENERAL INFORMATION:
APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kim
APPLICANT: Howes, Steven H.
APPLICANT: Resnick, Richard J.
APPLICANT: Gulukota, Kamalakar
APPLICANT: Gulukota, Kamalakar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-823-245A-30
                                                                                            Alignment Scores:
Pred. No.:
                                                                                                                                         US-09-823-245A-30
                                                                                                                                                                                 APPLICANT: Gulukota, Kamalakar
APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
TITLE OF INVENTION: POLYNUCLEGOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6401
CURRENT FILING LATE: 2001-03-29
PRIOR APPLICATION NUMBER: G0/194,941
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 631
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 30
LENGTH: 743
                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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100.00%
100.00%
52.95%
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
Query Match:
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                                                                                                         No . :
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APPLICANT: Rosen et al.
TITLE OF INVENTION: 47 Human Secreted Proteins
FILE REFERENCE: PC035P1
CURRENT APPLICATION NUMBER: US/09/895,298
CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: 09/591,16
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 1200-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: 60/113,006
PRIOR FILING DATE: 1999-12-18
PRIOR APPLICATION NUMBER: 60/112,809
PRIOR PILING DATE: 1998-12-17
NUMBER OF SEO ID NOS: 231
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 121
LENGTH: 966
TYPE: DNA
ORGANISM: Homo sapiens
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99.35%
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Conservative:
Mismatches:
Indels:
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APPLICANT: Moskal, Joseph
APPLICANT: Yamamoto, Hirotaka
APPLICANT: Yamamoto, Hirotaka
TITLE OF INVENTION: Detection and Treatment of
FILE REFERENCE: 97-186-E
CURRENT APPLICATION NUMBER: US/10/844,874
CURRENT FILING DATE: 2004-05-13
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
LENGTH: 2956
TYPE: DNA
OFFMARM: PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN PatentIN Pat
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; NAME/KEY: misc_feature
; OTHER INFORMATION: rat
US-10-844-874-19
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PRIOR APPLICATION NUMBER: 60/303828
PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 60/323380
PRIOR FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/361133
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: 60/36103
PRIOR PILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: 60/304016
PRIOR APPLICATION NUMBER: 60/304502
PRIOR FILING DATE: 2001-07-11
PRIOR FILING DATE: 2001-07-11
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Publication No. US20040029789A1
GENERAL INFORMATION:
APPLICANT: Anderson et al.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/188,186
CURRENT FILING DATE: 2002-07-02
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FILING DATE: 2001-07-09
APPLICATION NUMBER: 60/304502
FILING DATE: 2001-07-11
APPLICATION NUMBER: 60/305262
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PRIOR FILING DATE: 2001-07-13
PRIOR PELICATION NUMBER: 60/373881
PRIOR APPLICATION NUMBER: 60/305673
PRIOR APPLICATION NUMBER: 60/305673
PRIOR FILING DATE: 2001-07-16
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NUMBER OF SEQ ID NOS: 368
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                                                                                                                    etAlaTyrCysAspGlnIlePheGlnAspGluThrGlyLysAsnArgArgGlnSerGlyS
                                                                                                                                                                                   euLeuGlnLeuThrArgMetTyrProGlyLeuGlnValTyrThrPheThrGluArgMetM
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                                                                                                                                                           TGAAAAAGACAGTTGGTATCTATCCGAATGCCCAAATATACGTGACCACAGAGAAGCGCA
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Matches:
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APPLICANT: STEELMAND, KAITHEEN
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PRE
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
INUMBER OF SEQ ID NOS: 14084
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 11536
LENGTH: 3283
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzher
APPLICANT: Steinmann, Ka
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NAME/KEY: misc_feature
LOCATION: 1, 3283
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                                                                  AACTGGAC---TGTGACCTTTGTGCCATAGTGTCAAACTCAGGTCAGATGGTTGGCCAGA
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NUMBER OF SEQ ID NOS: 4096; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 380; LENGTH: 3207; TYPE: DNA; ORGANISM: Homo sapiens US-10-104-047-380
                                                                                                                                                                                                                                                                                                              Sequence 380, Application US/10104047
Publication No. US20030236392A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20030236392A1e1 fu
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
PRIOR FILING DATE:
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Best Local Similarity:
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 FILE REFERENCE: 21402-397C
CURRENT APPLICATION NUMBER: US/10/188,186
CURRENT APPLICATION NUMBER: US/10/188,186
CURRENT APPLICATION NUMBER: 60/303046
PRIOR APPLICATION NUMBER: 60/303046
PRIOR FILING DATE: 2001-07-05
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/360814
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: 60/303828
PRIOR FILING DATE: 2001-09-07
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                                                                                                                                                      Sequence 23, Application US/10188186
Publication No. US20040029789A1
GENERAL INFORMATION:
APPLICANT: Anderson et al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACTGGAC---TGTGACCTTTGTGCCATAGTGTCAAACTCAGGTCAGATGGTTGGCCAGA 425
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PRIOR FILING DATE: 2001-09-19
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: 60/304016
PRIOR APPLICATION NUMBER: 60/304016
PRIOR APPLICATION NUMBER: 60/304016
PRIOR FILING DATE: 2001-07-09
PRIOR PRIOR PRICATION NUMBER: 60/305262
PRIOR PRIOR PRICATION NUMBER: 60/305262
PRIOR FILING DATE: 2001-07-13
PRIOR PRICATION NUMBER: 60/373881
PRIOR FILING DATE: 2002-04-19
PRIOR PRICATION NUMBER: 60/305673
PRIOR PRICING DATE: 2001-07-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 368
SOPTWARE: CUstom
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Best Local Similarity:
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; LOCATION: (19)..(973)
US-10-188-186-23
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LENGTH: 1005
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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                                         536 TGAAAAAGACAGTTGGTATCTATCCGAATGCCCAAATATACGTGACCACAGAGAAGCGCA
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                                                                                                                                                                                                                                                                                                                                                        296 AGGTGGGAAATGAGATCGATCCTCCTGCATTTGGAGAATGAACAATGCCCCCACCA 355
    189
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                                                                                                                                                                                                                                                                                                                                                                                                                                      239 AACTGGAC---TGTGACCTTTGTGCCATAGTGTCAAACTCAGGTCAGATGGTTGGCCAGA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 ---GGCGGCCCCTTCGAACTCACTATGGATACATAAATGTGAAGACACAAGAGCCTTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 ACTGCTTTGGACAACCTGGTACAAAGTGGATACCATTCTCCTACACATACA-----
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                                                                                                                                                                                                                       alProLeuLeuLeuArgAsnTyrSerHisTyrPheGlnLysAlaArgAspThrLeuTyrM 149
etAlaTyrCysAspGlnIlePheGlnAspGluThrGlyLysAsnArg-------
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                                                                             euLeuGlnLeuThrArgMetTyrProGlyLeuGlnValTyrThrPheThrGluArgMetM 189
                                                                                                                  TTATTTGGGGACCTTTCCGCAATATGAGGAAAGATGGCAATGGCATCGTTTACAACATGT
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  Percent Similarity:
                                                      Alignment Scores
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PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/360814
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: 60/303828
PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 60/323380
PRIOR APPLICATION NUMBER: 60/323380
PRIOR FILING DATE: 2001-09-19
PRIOR PILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/361133
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: 60/304016
PRIOR FILING DATE: 2002-03-01
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
                                                                                                                                                                                                                              Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 368
SOFTWARE Custom
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19, Application US/10188186 Publication No. US20040029789A1 GENERAL INFORMATION:
                                                                                                               TYPE: DNA
ORGANISM: HOMO &
FEATURE:
NAME/KEY: CDS
LOCATION: (42)...
                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 60/304502
PRIOR FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 60/305262
PRIOR FILING DATE: 2001-07-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Anderson et al.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC FILE REFERENCE: 21402-397C
                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/305673
PRIOR FILING DATE: 2001-07-16
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CURRENT FILING DATE: 2002-07-02
                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/373881 PRIOR FILING DATE: 2002-04-19
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TGAGTTACTGTGATGGAGTTTTTTAAGAAGGAACTGGGAAGGACAGTGTATTATCTACAC
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Sequence 188, Application US/10097340 publication No. US20030087250A1 GENERAL INFORMATION:
APPLICANT: John MONAHAN APPLICANT: Manjula GANNAVARAPU
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TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
FILE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR APPLICATION NUMBER: 60/326,026
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-16
PRIOR APPLICATION NUMBER: 60/314,967
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR FILING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-19
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 188
LENGTH: 2048
                                                                                                                                                                                                                                                                                                                                                                                                                                                     365 ACCCAGCAGCGCCCCGGGGTCCCCCGCGGGACCGCCCACTGGACGGATACCTCGGAGTG
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Robert C. BAST,
Karen LU
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Rachel E. MEYERS
Michael MORRISEY
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Karen GLATT
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Shubhangi KAMATKAR
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APPLICANT: NAGALARI, KENJI

APPLICANT: MASUHO, YASUHIKO

TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA

FILE REFERENCE: 084335/0160

CURRENT APPLICATION NUMBER: US/10/094,749

CURRENT FILING DATE: 2002-03-12

PRIOR APPLICATION NUMBER: 60/350,435

PRIOR FILING DATE: 2002-01-24

PRIOR FILING DATE: 2001-09

PRIOR FILING DATE: 2001-09

PRIOR APPLICATION NUMBER: 60/350,435

PRIOR FILING DATE: 2001-09

PRIOR APPLICATION NUMBER: 02

PRIOR APPLICATION NUMBER: 02

PRIOR APPLICATION NUMBER: 02

PRIOR FILING DATE: 2001-09-14

NUMBER OF SEQ ID NOS: 3381

SOPTWARE: PATENTI VET: 2.1

SEQ ID NO 802

LENGTH: 2090

PRIOR HOMO 8apiens

ORGANISM: Homo sapiens
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Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
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US-10-094-749-802
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NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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; Sequence 31, Application US/10288252
Publication No. US20030143886A1
; GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: LAL, Preeti G.
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APPLICANT: DING, Li
TITLE OF INVENTION: TRANSFERASES
FILE REFERENCE: PI-0241 USA
CURRENT APPLICATION NUMBER: US/10/288,252
CURRENT FILING DATE: 2002-11-04
PRIOR APPLICATION NUMBER: DCT US01/30424
PRIOR FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: US 60/252,819
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: US 60/249,639
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: US 60/247,931
PRIOR APPLICATION NUMBER: US 60/247,931
PRIOR APPLICATION NUMBER: US 60/247,931
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/244,025
PRIOR APPLICATION NUMBER: US 60/244,025
PRIOR APPLICATION NUMBER: US 60/244,025
PRIOR APPLICATION NUMBER: US 60/238,481
PRIOR APPLICATION NUMBER: US 60/238,481
PRIOR APPLICATION NUMBER: US 60/236,523
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SEQ ID NO 31
LENGTH: 2075
TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030143686A1 2778782CB1
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WARREN, Bridget A.
YAO, Monique G.
TRIBOULEY, Catherine M
                                                                                           MetAsnGlnAlaProThrValGlyPheGluAlaAspValGlyGlnArgSerThrLeuArg 122
ValValSerHisThrSerValProLeuLeuLeuArgAsnTyrSerHisTyrPheGlnLys
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LEE, Ernestine A.
HAFALIA, April J.A.
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                                                                          ValPheSerArgTrpAlaLysLysArgProIleValPheAlaHisProSerTrpArgThr 301
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Search completed: December 22, 2004, 00:16:15
Job time : 610 secs

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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match
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1626
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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(without alignments)
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| 18.5 10.1 30 4 05-09-304-72 Sequence 12, April 18.5 9.1 90 3 US-09-304-601-23 Sequence 22, April 18.5 9.1 90 3 US-09-304-601-23 Sequence 22, April 18.5 9.1 90 3 US-09-304-601-26 Sequence 22, April 18.5 9.1 90 3 US-09-304-601-26 Sequence 22, April 18.6 9.2 90 1 US-09-905-7 Sequence 22, April 18.6 9.2 91 US-09-905-7 Sequence 22, April 18.6 9.2 91 US-09-905-7 Sequence 22, April 18.6 9.2 91 US-09-905-7 Sequence 22, April 18.6 9.2 91 US-09-905-7 Sequence 22, April 18.6 9.2 91 US-09-905-7 Sequence 21, April 18.6 9.2 91 US-09-905-7 Sequence 21, April 18.6 9.2 91 US-09-102-385G-12 Sequence 21, April 18.6 9.2 91 US-09-102-385G-12 Sequence 21, April 18.6 9.2 91 US-09-102-385G-12 Sequence 21, April 18.6 9.2 91 US-09-102-385G-12 Sequence 21, April 18.6 9.2 91 US-09-102-385G-12 Sequence 21, April 18.6 9.2 91 US-09-102-385G-12 Sequence 22, April 18.6 9.2 91 US-09-102-385G-12 Sequence 23, April 18.6 9.2 91 US-09-102-385G-15 Sequence 23, April 18.6 9.2 91 US-09-102-385G-15 Sequence 23, April 18.6 9.2 91 US-09-102-385G-15 Sequence 23, April 18.6 9.2 91 US-09-102-385G-15 Sequence 23, April 18.6 9.2 91 US-09-102-385G-15 Sequence 23, April 18.6 9.2 91 US-09-102-385G-15 Sequence 23, April 18.6 9.2 91 US-09-102-385G-15 Sequence 23, April 18.6 9.2 91 US-09-102-385G-15 Sequence 23, April 18.6 9.2 91 US-09-102-385G-15 Sequence 23, April 18.6 9.2 91 US-09-102-385G-15 Sequence 23, April 18.6 9.2 91 US-09-102-31 US-09-31 US   | DЪ  | 8   | B 8   | D Q  | Qy   | Quer<br>Best<br>Matc  | RESULI<br>US-09-<br>Sequence of the control of the cont |            | 10 00 00 00 00 00 00 00 00 00 00 00 00 0  | 228   |
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241 EKSHPSVPYHYFEKGRLDECQMYLAHEQAPRSAHRFITEKAVFSRWAKKRPIVFAHPSWR 300

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APPLICANT: Kapitonov, Dmitri
APPLICANT: Yu, Robert
TITLE OF INVENTION: NOVEL SIALYLTRANSFERASES
FILE REFERENCE: VCUIP-6
CURRENT APPLICATION NUMBER: US/09/334,601
CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 94
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
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                                                                                                   TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13, Application Patent No. 6280989
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     Sequence 3915, Application US/09621976 Patent No. 6639063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 39.3%; Score 639.5; DB 3; Length 336; Best Local Similarity 47.9%; Pred. No. 1.1e-61; Matches 125; Conservative 44; Mismatches 89; Indels 3
                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                             APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Jobert, S. APPLICANT: Giordano, J.Y.
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TYPE: PRT
                                                 TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: SIGNAL LOCATION: -18..-1
                                   FEATURE:
                                                                                    ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLCEBIVVYGMVSDSYCREKSHPSVPYHYFEKGRLDECQMYLAHEQAPR-SAHRFITEKA 281
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Best Local (
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                                                                                                                                                               APPLICATION NUMBER: US/08/446,875
PRING DATE: July 12, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/102,385
PILING DATE: August 4, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 111-197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 59
OTHER INFORMATION: X
NAME/KEY: UNSURE
LOCATION: 56
OTHER INFORMATION: X
NAME/KEY: UNSURE
                                                                                                TELEFAX: (310) 277-129
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
MOLECULE TYPE: protein -446-875-16
                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE PATENTIA PERSON
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS: Pone, Smith, Lande & Rose
ADDRESSEE: Pone, Smith, Lande & Rose
STREET: 2029 Century Park East, Suite 3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Burlingame, Alma L.
APPLICANT: Medzihradszky, Katalin
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Identification and Synthesis of Sialyltransferases
                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 90067
                                                 TYPE: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                             TOPOLOGY:
                                                                                                                              TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKAPGRIVLIIICSVVFSAVYILLCCWAGLPLCLATCLDHHFPTGSRPTVPGPLHFSGYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92;
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USA
                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08446875
                                                             340 amino acids
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Gillespie, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kelm, Sorge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wen, Xiaohong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Paulson,
                                                                                                                                (310)
                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
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                                                                                                                  277-1297
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                                                                                                                                 788-5000
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                                                                                                  16:
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Pred. No. 1.7e-46;
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US-08-503-133A-2
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WATERIT NO. 5/1/2-1
GENERAL INFORMATION:
APPLICANT: Gerardy-Schahn, Rita; Fukuuu,
APPLICANT: Nakayama, Jun; Eckhardt, Matthias
APPLICANT: Nakayama, Jun; Eckhardt, Matthias
APPLICANT: Nakayama, Jun; Eckhardt, Matthias
APPLICANT: Nakayama, Jun; Eckhardt, Matthias
APPLICANT: Nakayama, Jun; Eckhardt, Matthias
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APPLICANT: Nakayama, Jun; Eckhardt, Matthias
APPLICANT: Nakayama, Jun; Eckhardt, Matthias
APPLICANT: Nakayama, Jun; Eckhardt, Matthias
APPLICANT: Nakayama, Jun; Eckhardt, Matthias
APPLICANT
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                                                                                                                                                               Query Match
Best Local
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Best Local
                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/503,133A
FILING DATE: 17-JULY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/04289
FILING DATE: 22-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 838-3884 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                   TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Hanson, No. 5747326man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 121-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
125 HSLLPEVSPMKNRRFKTCAVVGNSGILLDSGCGKEIDSHNFVIRCNLAPVVBPAADVGTK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 DSYCREKSHPSVPYHYFE 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 YPGLQVYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALBLCBEIVVYGMVS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 LRNYSHYFQKARDTLYMVWGQGRHMD-----RVLGGRTYRTLL------QLTRM 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 CRRCAVVGNSGNLRESSYGPEIDSHDFVLRMNKAPTAGFEADVGTKTTHHLV-----
                                                              59 YSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQR 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55;
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                                                                                                                                                                                                                                                                                                                                     amino acid
GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DS--KGNWH-----HYWE 302
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                                                                                                                                                                                                                                                                                                                                                                                                    359 amino acids
                                                                                                                            12.1%; Score 196.5; DB 1 ilarity 27.5%; Pred. No. 6.4e-13; Conservative 39; Mismatches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diskette, 3.5 inch, 360 kb storage
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Pred. No. 3.6e-13;
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                                                                                                                                                                                           DB 1;
                                                                                                                                98;
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                                                                                                                                                                                              Length 359;
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                                                                                                                                                     US-08-576-775A-2
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                                                                                                             Query Match
                                                                                                                                                                                                                                                                   TELEFAX: (212) 838-3884 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Gerard
                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 22-December-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/50 FILING DATE: 17-July-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Nakayama TIITLE OF INVENTION: TIITLE OF INVENTION: TIITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/576,775A
FILING DATE: 21-December-1995
CLASSIFICATION: 514
                                                                                             Local
                                                                                                                                                                                                                                                                                                                                             NAME: Hanson, No. 5849904max REGISTRATION NUMBER: 30,946 REFERENCE/DOCKET NUMBER: BOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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125 HSLLPEVSPMKNRRFKTCAVVGNSGILLDSGCGKEIDSHNFVIRCNLAPVVEFAADVGTK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 TYRTLLQLTRMYPGLQV-----YTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTM 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 STLRVVSHTSVPLL---LRNYS------HYFQKARDTL----YMVWGQGRHMDRVLGGR
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                             59 YSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGABIDSAECVFRMNQAPTVGFEADVGQR 118
                                                                                             Similarity
                                                                                                                                                                                       amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLATRECDETHLYGEW--PEPKDLNGKAVKYHYYD---
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                                                                                                                                                                                                                               359 amino acids
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NVENTION: Isolated Polysialyl Transferases,
NVENTION: Nucleic Acid Molecules Coding Therefor, Methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Felfe & Lynch
                                                                                                                                                                                                                                                                                                                                                                                     No. 5849904man D.
                                                                       12.1%; Score 196.5; DB 2
27.5%; Pred. No. 6.4e-13;
tive 39; Mismatches 98
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                                                                                                             DB 2;
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                                                                                                             Length 359;
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                                                                                                             US-08-972-498-2
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                                    Matches
                                                                      Query Match
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                                                                                                                                                                                                                      TELEFAX: (212) 838-38 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gerardy-Eduam, Nathias
APPLICANT: Nakayama, Jun; Eckhardt, Matthias
TITLE OF INVENTION: Isolated Polysialyl Transferases,
TITLE OF INVENTION: Nucleic Acid Molecules Coding Therefor, Methods of
                                                                                                                                                                                                                                                                        NAME: HANSON, NO. 5959078man D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1
TELECOMMUNICATION INFORMATION:
                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 22-December-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 17-July PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 08/576,775
FILING DATE: 21-December-1995
APPLICATION NUMBER: 08/503,133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
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ADDRESSEE: Felfe & Lynch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PS/
OPERATING SYSTEM:
                                                     Local Similarity
                                                                                                                                               TYPE: ami
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                                                                                                                                                                                                                                                        TELEPHONE:
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59 YSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQR 118
                                    ; 69
                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STLRVVSHTSVPLL---LRNYS-----HYFQKARDTL----YMVWGQGRHMDRVLGGR 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       805 Third Avenue
                                                                                                                                                                                    359 amino acids
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                                      Conservative
                                                                                                                                                   linear
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                                                                                                                                                                                                                                                            (212) 688-9200
                                                                                                                              protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     536
                                                                                                                                                                                                                                         838-3884
                                    12.1%; Score 196.5; DB 2; 27.5%; Pred. No. 6.4e-13; tive 39; Mismatches 98;
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                                                                      Length 359;
                                      Indels
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                                      45;
                                      Gaps
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US-08-899-545-2
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                                                                       Matches
                                                                                          Query Match
Best Local
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APPLICANT: Gerard
APPLICANT: Nakaya
                                                                                                                                                                                                      TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 5EQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PS/4
COMPUTER: IBM PS/4
OPERATING SYSTEM: PC-DOS
SOFTWARB: Wordperfect
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/899,545
                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & L
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 805 Third Avenue CITY: New York City
                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                       NAME: Hanson, No. 60 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                     Local Similarity
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                                 59 YSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQR 118
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HSLLPEVSPMKNRRFKTCAVVGNSGILLDSGCGKEIDSHNFVIRCNLAPVVEFAADVGTK 184
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Nakayama, Jun; Eckhardt, Matthias
WENTION: Isolated Polysialyl Transferases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                       Conservative
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                                                                                        12.1%;
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                                                                                                                                                                                                                                                                                                                        BOER 1050
                                                                                        Score 196.5; DB 3
Pred. No. 6.4e-13;
                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 kb storage
                                                                                                          DB 3;
                                                                         ; 86
                                                                                                        Length 359;
                                                                         Indels
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                                                                       45;
                                                                       Gaps
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Query M

LD NO:
....ACTERISTICS:
343 amino acids
arpE: amino acid
TOPOLOGY: linear
; MOLECULE TYPE: pro-
US-08-446-875-2
Query M
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US-08-446-875-2
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                                                                                                                                                                                                                                                                                            ATTORNEI, COLORDA DAVIGO DAVIGO DAVIGO DAVIGO DE LA COLORDA DAVIGO DAVIGO DA CASTO NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 111-197
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1788-5000
TELECOMMUNICATION 1777-1297
                                                                                                                                                                                                                                                                               TELEFAX: (310) 277-1297 INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/1 FILING DATE: August 4, 1 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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ADDRESSEE: Poms, Smi
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                                                                          y Match 11.7%; Score 191; DB 2; Length 343:
Local Similarity 30.0%; Pred. No. 2.4e-12;
hes 57; Conservative 36; Mismatches 77; Indels
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STATE: CA
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133 PLLEKRLVSCRRCAVVGNSGNLKESYYGPQIDSHDFVLRWNKAPTEGFEADVGSKTTHHF 192
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                      PLVRE---PCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRSTLRV 123
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2029 Century Park East, Suite 3800
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Medzihradszky, Katalin
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Gillespie, William
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Wen, Xiaohong
Wen, Siaohong
Brian Duane
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4, 1993
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US-08-102-385G-2
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MOLECULE TYPE: protein
US-08-102-385G-2
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                                                                                                                                        Matches
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ETLING DATE: 04-AUG-1992
ATTORNEY_AGENT INFORMATION:
NAME: Oldenkamp_David_J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 97-062
TELECOMMUNICATION INFORMATION:
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APPLICANT: Paulson
APPLICANT: Wen, X
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 343 amino acid
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FILING DATE: 04-AUG-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Identification and Synthesis of Sialyltransferases
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CITY: Los Angeles
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                                                                                                                                        Local Similarity 30.0
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124 VSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQVYT 183
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                                                           133 PLLEKRLVSCRRCAVVGNSGNLKESYYGPQIDSHDFVLRNNKAPTEGFEADVGSKTTHHF 192
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Livingston, Brian Duane
Gillespie, William
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                                                                                                                                      11.7%; Score 191; DB 2; I
30.0%; Pred. No. 2.4e-12;
ative 36; Mismatches 77;
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US-08-626-994A-3
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: 1.44 di
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                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Arnold Turk
REGISTRATION NUMBER: 33,094
REFERENCE/DOCKET NUMBER: P1
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FILING DATE: April 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Virginia COUNTRY: U.S.A.
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                                  221
                                                                 212 SATVTRTL----VDFFVEHRGQLKVQLAWPGNIMQHVNRYWKNKHLSPKRLSTGILMYTL
                                                                                                169 LLQLTRMYPGLQVYTFTER-----WMAYCDQIFQ--DETGKNRRQSGSFLSTGWFTMIL 220
                                                                                                                                         165
                                                                                                                                                                      120 TLRVVSHTSVPLLLRNYSHYFQKARDTL------YMVWGQGRHMDRVLGGRTYRT 168
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                             ALELCEEIVVYGMVS---DSYCREKSHPSVPYHYFEK 254
                                                                                                                                       NLT----TFNPSILEKYYNNLLTIQDRNNFFLSLKKLDGAILW-----IPAFFFHT
                                                                                                                                                                                                          SLLPDVSPIMNKRYNVCAVVGNSGILTGSQCGQEIDKSDFVSRCNFAPTEAFHKDVGRKT
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ASAICEEIHLYGFWPFGFDPNTRE----DLPYHYYDK 300
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1941 Roland Clarke Place
                                                                                                                                                                                                                                                                                                                                                                                                                     339 amino acids
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VENTION: Sia' 2,3Gala 1,4GlcNAc '
VENTION: SIALYLTRANSFERASE
                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                   not relevant
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3, 1996
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RESULT 12
US-08-957-742-3
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Best Local Similarity
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APPLICATION NUMBER: 08/626,994
FILING DATE: April 3, 1996
APPLICATION NUMBER: JP 77469/1995
FILING DATE: April 3, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold Turk
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                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 3:
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ADDRESSEE: Greenblum & Bernstein, P.L.C
STREET: 1941 Roland Clarke Place
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1+ (ASCII)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Reston
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                        TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 33,094
REFERENCE/DOCKET NUMBER: P14595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELEPHONE:
                                                                                                                                                                                                105 SILPDVSPIMNKRYNVCAVVGNSGILTGSQCGQBIDKSDFVSRCNFAPTBAFHKDVGRKT 164
                                                                                             169 LLQLTRMYPGLQVYTFTER-----MMAYCDQIFQ--DETGKNRRQSGSFLSTGWFTMIL
                                                                                                                                                               120 TLRVVSHTSVPLLLRNYSHYFQKARDTL-----YMVWGQGRHMDRVLGGRTYRT 168
268
                                                                                                                                  165 NLT----TFNPSILEKYYNNLLTIQDRNNFFLSLKKLDGAILW--
                                                                                                                                                                                                                              60 SVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRS 119
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                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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                                                             SATVTRTL----VDFFVEHRGQLKVQLAWPGNIMQHVNRYWKNKHLSPKRLSTGILMYTL
                              ALELCEEIVVYGMVS---DSYCREKSHPSVPYHYFEK 254
ASAICEBIHLYGFWPFGFDPNTRE----DLPYHYYDK 300
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VENTION: Sia' 2,3Gala 1,4GlcNAc ' 2,8-

VENTION: SIALYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                        339 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (703)
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                                                                                                                                                                                                                                                                                                                                                   ss: not relevant
linear
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                                                                                                                                                                                                                                                                   Score 190.5; DB:
Pred. No. 2.7e-12;
8; Mismatches 81
                                                                                                                                                                                                                                                                                                         DB 3;
                                                                                                                                                                                                                                                                                                         Length 339;
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                                                                                                                                         ----IPAFFFHT 211
                                                                                                                                                                                                                                                                           43;
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US-08-626-994A-1 RESULT 13

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Sequence 1, Application US/08626994A Patent No. 5798244 GENERAL INFORMATION:

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Matches
                                                                                                                                       Sequence 1, Application US/08957742
Patent No. 6017743
GENERAL INFORMATION:
APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION: Sia 2,3Gala 1,4G1cNAC 'TITLE OF INVENTION: SIALYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1+ (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/626,994A
FILING DATE: APPLI 3, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 77469/1995
FILING DATE: APPLICATION: 435
PRIOR APPLICATION NUMBER: JP 77469/1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold Turk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (703) 716-1180 INFORMATION FOR SEQ ID NO: 1:
STREET: ...
STREET: ...
CITY: Reston
Virginia
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                                                                                                 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION
TELEPHONE: (703) 716-1191
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MEDIUM TYPE: 1.44 di
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ADDRESSEE: Greenblum
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 11.7%; Score 190.5; DB 1; Local Similarity 30.0%; Pred. No. 3e-12; hes 65; Conservative 28; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 364 amino acids
TYPE: amino acid
STRANDEDNESS: not relevi
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STATE: Virginia
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                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                   293 ASAICEEIHLYGFWPFGFDPNTRE----DLPYHYYDK 325
                                                                                                                                                                                                                                                                                                                                                                                         221 ALELCEEIVVYGMVS---DSYCREKSHPSVPYHYFEK 254
                                                                                                                                                                                                                                                                                                                                                                                                                               237 SATVTRTL----VDFFVEHRGQLKVQLAWPGNIMQHVNRYWKNKHLSPKRLSTGILMYTL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 NLT----TENPSILEKYYNNLLTIQDRNNFFLSLKKLDGAILW-----IPAFFFHT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 LLQLTRMYPGLQVYTFTER-----MMAYCDQIFQ--DETGKNRRQSGSFLSTGWFTMIL 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 SSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMVQAPTVGFEADVGQRS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3E: Greenblum & Bernstein, P.L.C
1941 Roland Clarke Place
                                                             E: Greenblum & Bernstein, P.L.C
1941 Roland Clarke Place
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VENTION: Sia' 2,3Gala 1,4G1cNAc '
VENTION: SIALYLTRANSFERASE
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Sequence 6, Application US/08666367B Patent No. 5854042
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APPLICATION NUMBER: 08/626,994
FILING DATE: April 3, 1996
APPLICATION NUMBER: JP 77469/1995
FILING DATE: April 3, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold Turk
                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Shuich
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OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1+ (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,742
                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44
                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 di
                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
  OPERATING SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 33,094
REFERENCE/DOCKET NUMBER: P1
                                                                                                                                                                               CITY: Washington
                                               COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 SILPDVSPIMNKRYNVCAVVGNSGILTGSQCGQBIDKSDFVSRCNFAPTEAFHKDVGRKT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293 ASAICEEIHLYGFWPFGFDPNTRE----DLPYHYYDK 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 SATVTRTL----VDFFVEHRGQLKVQLAWPGNIMQHVNRYWKNKHLSPKRLSTGILMYTL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 LLQLTRMYPGLQVYTFTER------MMAYCDQIFQ--DETGKNRRQSGSFLSTGWFTMIL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 NLT----TFNPSILEKYYNNLLTIQDRNNFFLSLKKLDGAILW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 TLRVVSHTSVPLLLRNYSHYFQKARDTL-----YMVWGQGRHMDRVLGGRTYRT 168
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                                                                                                               20005
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                                                                                                                                                              D.C
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                                                                                                                                                                                                                                                                                                Shuichi TSUJI et al.
VENTION: NOVEL SUGAR-CHAIN SYNTHETASE AND PROCESS FOR
VENTION: PRODUCING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U.S.A.
                       SYSTEM:
                                                                                                                                      U.S.A.
SYSTEM: MS-DOS
Wordperfect 5.1
                                          IBM Compatible
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IBM PC compatible
SYSTEM: MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.7%; Score 190.5; DB 3; 30.0%; Pred. No. 3e-12; tive 28; Mismatches 81;
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TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGIH: 355 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-666-367B-6
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Search completed: December 10, 2004, 18:26:42 Job time : 40 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/666,367B
FILING DATE: AUGUST 19, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WATTEN M. Cheek, Jr.
REFERENCE/DOCKET NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                  333 FNLEKQVWKR 342
                                                                                                                                                                                                                                             231 FLNYYGRRPRERFDEDFTWNKYLVAHPDFL---RYLKNRFLKSKNLQKPYWRLYRPTTGA 287
                                                                                                                                                                                                                                                                                   182 ------YTFTERMMAYCDQIFQDETGKNRRQSGSFL------STGW 215
                                                                                                                                                                                                                                                                                                                           186 LONLGHKGFKKI------POGKHI-----RYIHFLEAVRDYEWLKALLLDKDIRKG 230
                                                                                                                                                                                                                                                                                                                                                                                                       216 FTMILALELCEEIVVYGMVSDSYCREKSHPSVPYHYFEKGRLDECQMYLAHEQAPRSAHR 275
                                                                                                                                                                                                                                                                                                                                                                 133 LRNYSHY-FOKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQV------ 181
                                                                                                                        276 FITEKAVFSR 285
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